GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen

Ltd

12 13 14 15 16 17

```
Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Run
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM protein -
        54
55
56
57
11
11
                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                          Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A_Geneseq_032802:*
1: /SIDS1/gcgdata/h
2: /SIDS1/gcgdata/h
3: /SIDS1/gcgdata/h
                                                                                                                                                                                                                                      Query
Match
        110:
111:
113:
114:
115:
116:
116:
119:
120:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   June 10, 2002; 15:18:20 ; Search time 73.49 Seconds (without alignments) 21.160 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             747574 segs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-647-522-1
72
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1989.DAT:*
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1990.DAT:*
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1992.DAT:*
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1992.DAT:*
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1992.DAT:*
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:*
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:*
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:*
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1997.DAT:*
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1998.DAT:*
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GEIQTKPDRVGQAT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               />+DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1984.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1985.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1986.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1987.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1983.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1988.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:*
                                                                                                                                                                                                                                        Length
    14
450
300
59
257
258
283
913
1997
1997
                                                                                                                                                                                                                                          멂
    AAU55446
ABG06177
ABG05880
AAB54021
AAB76594
AAB19774
AAM78821
AAM79805
                                                                                                                                                                                                                                          H
                                                                                                                                                           AAY33648
AAY33651
ABB69651
                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           747574
Novel human diagno
Novel human diagno
Human pancreatic c
Corynebacterium gl
Human protein tyro
Human protein SEQ
Human protein SEQ
                                                                                                                                                                                                                                      Description
                                                                                                                                     Propionibacterium
                                                                                                                                                       Drosophila melanog
                                                                                                                                                                           C. rastonii hemoly
```

Peptide #352 encod	AAM13918	22	206	50.0	36	
₹	AAM66049	22	206	0	36	
Human brain expres	AAM53666	22	206	0	36	
#34	ABB18345	22	206	0	36	
#369	ABB32863	22	206	0	36	
eptide	ABB27693	22	206	0	36	
#	AAM05553	22	67	0	36	
#4	AAM30410	22	67	0	36	
Peptide #4334 enco	AAM17900	22	67	50.0	36	
one m	AAM70074	22	67	0	36	
Human brain expres	AAM57667	22	67	0	36	
#4	ABB22248	22	67	0	36	
4	ABB36928	22	67		36	
#435	ABB31708	22	67		36	
#	AAM04674	22	53	50.0	36	
500	AAM29463	22	. 53	0	36	
# 3	AAM16974	22	53	0	36	
ne ma	AAM69142	22	53	0	36	
ain ex	AAM56761	22	53	0	. 36	
#3369	ABB21370	22	53	0	36	
	ABB35960	22	53	0	36	
#3434	ABB30783	22	53	0	36	
hite	AAG85010	22	931		37	
Novel human diagno	ABG00217	22	876	51.4	37	
teri	AAY04839	20	505		37	
Murine NNX3 protei	AAY50875	21	457		37	
el human dia	ABG27128	22	359		37	
0 14	AAW98829	19	339	$\dot{\mathbf{L}}$	37	
Helicobacter pylor	AAW72879	19	280		. 37	
ynebacteri	AAB80049	22	250	51.4	37	
C glutamicum prote	AAG90023	22	250		37	
Propionibacterium	AAU62661	22	144	51.4	37	
pionibacte	AAU46616	22	122	51.4	. 37	
C glutamicum prote	AAG92485	22			38	

ALIGNMENTS

40

RESULT
AAX30648
ID AAX3
XX AAX3
AC AAX3
AC AAX3
AC CAY
XX.
DE C.r
AXX.
LEE C.r
AXX

KW trea
AXX CAY
AXX

CAY
AXX

COMPAN

COMP WO9950294-A1. Carybdea rastonii. Hemolytic protein; blood platelet agglutination; drug development; treatment; sting; jellyfish; pharmaceutical; pesticide. C. rastonii hemolytic protein derived 06-JAN-2000 01-APR-1998; 30-MAR-1999; 07-OCT-1999. AAY33648; AAY33648 standard; peptide; (SUNR) SUNTORY LTD. Н (first entry) 98JP-0088569. 99WO-JP01607 14 Ą peptide

mechanism Protein with hemolytic activity, useful for drugs treating jelly fish stings, pharmaceuticals with blood platelet agglutination activity, setticides by use of the hemolytic activity, and study of the hemolytic activity.

WPI; 1999-580740/49.

Nagai H,

Nakajima T;

Ş 멍

1 GEIQTKPDRVGQAT

14

Best Local Similarity 100 Matches 14; Conservative

100.0%;

0;

pred. No. 0.00018;
; Mismatches 0;

Indels

0

Gaps

0

```
RESULT
AAY33651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 14
                                                          This invention describes a novel protein which has hemolytic activity, blood platelet agglutination activity and a molecular weight of about 50,000 Da (by SDS-PAGE). The protein, homologs and analogs of the invention can be used as a novel approach to developing drugs useful for the treatment of jelly fish stings, pharmaceuticals with blood platelet agglutination activity, pesticides by use of the hemolytic activity, and in the study of the hemolytic mechanism. This sequence represents the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel protein which has hemolytic activity, blood platelet agglutination activity and a molecular weight of about 50,000 ba (by SDS-PAGE). The protein, homologs and analogs of the invention can be used as a novel approach to developing drugs useful for the treatment of jelly fish stings, pharmaceuticals with blood platelet agglutination activity, pesticides by use of the hemolytic activity, and in the study of the hemolytic mechanism. AAY33648-Y33650 represent fragments of the hemolytic protein described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hemolytic
Sequence
                                                                                                                                                                                                                               Claim 4; Page 26-27; 32pp; Japanese
                                                                                                                                                                                                                                                                                  Protein with hemolytic activity, useful for drugs treating jelly fish stings, pharmaceuticals with blood platelet agglutination activity, pesticides by use of the hemolytic activity, and study of the hemolytic mechanism.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Nagai H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SUNR ) SUNTORY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9950294-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carybdea rastonii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C. rastonii hemolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY33651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY33651 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N
                                                                                                                                                                                                                                                                                                                                                                                               1999-580740/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GEIQTKPDRVGQAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            geiqtkpdrvgqat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 100
l4; Conservative
                                                                                                                                                                                                                                                                                                                                                                              AAZ23610.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Nakajima T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page
                                        protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein; blood platelet agglutination; drug development;
sting; jellyfish; pharmaceutical; pesticide.
450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98JP-0088569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-JP01607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32pp;
                                          described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .0%;
                                        in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 72; DB
Pred. No. 6.2
); Mismatches
                                        the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ጅ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 20,
6.2e-06;
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
```

Š

Дb

8 x 0 0 0 0 0 0 0 0 x 8

Query Match

100.0%;

Score

72;

DB 20;

Length

450;

RESULT AAU55446

4

망 Ş

ΧIJ

AAU55446 standard; Protein; 59

B

```
RESULT
ABB69651
                                                             Query Match
Best Local S
Matches 8
                                                                                                                                                                                                                         useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                          The sequence data for this patent did not form specification, but was obtained in electronic i
                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention
                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 35745; 21pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-656860/75.
N-PSDB; ABL13754.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-MAR-2000;
11-JUL-2000;
                                                                                                                                             Sequence
                                                                                                                                                                            at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                          genes
                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB69651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB69651
   123
                                                                                                                                                                                                                                                                                                                                                                                                         interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PEKE ) PE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 geigtkpdrvggat 69
                                N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  w
kmqtkvdavgqit 135
                                EIQTKPDRVGQAT
                                                                                                                                                                                                                                                                                                                                                                                                            from Drosophila and actions .
                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                               300 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   developmental
                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-191637P
2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Z
                                14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein;
                                                                              54.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ľ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                      detection reagent for detecting 1000 for elucidating cell signalling and c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   biology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300
                                                                              Score 39; DB
Pred. No. 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Myers
                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ξ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   signalling;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ID NO 35745
                                                                                              22;
                                                                ω
--
                                                                                                                                                                                            format directly from
                                                                                            Length 300
                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     insecticide;
                                                                                                                                                                                                                                                                                                                                                                        English.
                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                          cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                         or more
                                                                Gaps
                                                                                                                                                                                                                                                                                                         and
                                                                                                                                                                                             WIPO
                                                                                                                                                                                                                                                                                                                          si
                                                               0
```

```
ABG06177
                                                                                                                                                                                 В
                                                                                       Š
                            RESULT
                                                                                                                                                                                                               pusulosis, hypertosis and osteomyelitis), weitis and endophthalmitis.

P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The conspective for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and country of the antibodies may also be used as consequence in the determining P. acnes polypeptides and country of the sequence data for this patent did not form part of the printed consequence data for this patent did not format directly from WIPO
                                                                                                                             Query Match
Best Local
                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-APR-2000;
02-JUN-2000;
07-JUL-2000;
 ABG06177 standard; Protein; 257
                                                                                                                                                                                                                                                                                                                                                                                                                 the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Propionibacterium acnes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L'maisonneuve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200181581-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Propionibacterium acnes immunogenic protein #16342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptides. The proteins and their associated DNA sequences are used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-APR-2001; 2001WO-US12865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU55446
                                                                16
                                                                             4 QTKPDRVGQAT 14
||:| | || |
                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences
                            s
                                                                                                                Similarity 63. 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; SEQ ID No 16641; 1069pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Persing DH, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-199047P.
2000US-208841P.
2000US-216747P.
                                                                                                                                                                               AA;
                                                                                                                           52.8%;
63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mitcham JL, Wang
, Jen S, Carter
                                                                                                              Score 38; DB Pred. No. 22; 1; Mismatches
  ⋧
                                                                                                                           DB
22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SS,
                                                                                                                                       Length 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bhatia
                                                                                                                Indels
                                                                                                                0;
                                                                                                                Gaps
                                                                                                                0
ABG05880
                                                                           В
                                                                                                 δÃ
```

```
Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical
                                                                                                                                                                                                                                                                                                                                                                                                                         and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences fithe invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from William at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; chromosome mapping; gene mapping; gene therapy; forensic
food supplement; medical imaging; diagnostic; genetic disorder
                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human diagnostic protein #6168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG06177;
                                                                                          19
                                                                                                                    2 EIQTKPDRVGQAT 14 : |: | | | | |
σ
                                                                                kirvkpdrtgvvt 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-639362/73
DB; AAS70364.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20; SEQ ID No 36536; 103pp; English.
                                                                                                                                                                                                           Similarity
7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RT,
                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0540217
2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liu C,
                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tang
                                                                                                                                                                                                                                     Score 38;
Pred. No.
                                                                                                                                                                                                                                 DB
92;
                                                                                                                                                                                                                                                                     Length 257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ion of mutations and to assess
                                                                                                                                                                                                           Indels
                                                                                                                                                                                                           0
```

ABG05880 standard; Protein;

ABG05880;

```
AC XX
                                                AAB54021
                                                                RESULT
                                                                                                                 밁
                                                                                                                                             Ş
                                                                                                                                                                                                                                                                                                                                          CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC polymucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC to restore normal activity of (II) or to treat disease states involving CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC diagnostics amino acid sequences. ABG00010-ABG30377 represent novel human CC diagnostic amino acid sequences of the invention.
                                                                                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
AAB54021;
                                 AAB54021 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drmanac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-FEB-2002
                                                                                                                                                                                                                                                                                              Note: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-OCT-2001
                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               food
                                                                                                                 19
                                                                                                                                                 2 EIQTKPDRVGQAT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                 kirvkpdrtgvvt 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-639362/73
)B; AAS70067.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human diagnostic protein #5871
                                                                                                                                                                                7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID
                                                                                                                                                                                                                                                                    258
                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36239; 103pp; English.
                                                                                                                                                                                                52.8%;
53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ΥT
                                 283
                                                                                                                                                                                                Score 38; DB
Pred. No. 92;
                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                 22;
                                                                                                                                                                                4.
                                                                                                                                                                                                               Length 258;
                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                     printed
from WIPO
                                                                                                                                                                                Gaps
                                                                                                                                                                                  0,
```

RESULT AAB76594

δÃ 밁

47 kirvkpdrtgvvt 59 2 EIQTKPDRVGQAT

Query Match Best Local Matches

Similarity 7; Conserv

Conservative

52.8%;

Score 38; DB 21 Pred. No. 1e+02;

21;

Length 283

Indels

0,

Gaps

.0

Mismatches

```
cc gynaecological, cardiant and antiinflammatory activities, and can be used con in gene therapy. The polynucleotide and proteins can be used for corrections, treating, or ameliorating a medical condition or in assays cfor diagnosing a pathological condition or a susceptibility to one in a complete. Binding partners to the proteins and the activity of the proteins can be identified. The pancreatic cancer antigens can be used to detect, treat or prevent pancreatic disorders, especially cancer.

Cc Agonists and antagonists to the antigens can be screened for The pancreatic cancer antigens can be used to design nucleic candity by a concertant disorders, especially cancer the cancer antigen polynucleotides can be used to design nucleic candity by addition probes that can be used in chromosome mapping, linkage and diagnostic methods. The proteins can be used to generate antibodies which are used to purify, detect and target the polypeptides, including both in vivo and in vitro diagnostic and therapeutic methods. The proteins can be used to treat or prevent neural, immune system, muscular, corrections and contractions and contractions and contractions are used to treat or prevent neural, immune system, muscular, corrections are sentential culturary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antiinflammatory; cardiant; gene therapy; chromosome mapping; linkage analysis; tissue identification; tissue typing; forensic neural; immune system; muscular; reproductive; gastrointestinal;
                                                                                                                                                                                                                                                                                                                                                                                                                                             proteins, called pancreatic cancer antigens, given in AAB54008 AAB54466. The human pancreatic cancer antigens have cytostatic, neuroprotective, nootropic, immunomodulatory, relaxant, contrac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nootropic; immunomodulatory; relaxant; contraceptive; gynaeco antiinflammatory; cardiant; gene therapy; chromosome mapping;
Sequence
                                              sequences used in the exemplification
                                                                   reproductive, gastrointestinal, pulmonary, cardiovascular, renal or proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC98773 to AAC99231 encode the human pancreatic cancer associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; Page 909-910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-579444/54.
N-PSDB; AAC98786.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-MAR-2000; 2000WO-US05989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200055320-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pulmonary; cardiovascular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human pancreatic cancer antigen protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-SEP-2000
    283 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9905-0124270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pancreatic cancer; pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1379pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ancreatic cancer antigen; cytostatic; neuroprotect
                                                   of the
                                              present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                   relaxant, contraceptive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gynaecological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NO:473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
```

0,

```
Corynebacterium glutamicum nucleic acids encoding membrane construction and membrane transport proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers for transformation .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corynebacterium glutamicum; brevibacterium lactofermentum; MCT; membrane construction and membrane transport protein; petroleum spill; hydrocarbon degradation; gram positive aerobic bacterium; marker; identification; microorganism; fine chemical production; transformation;
                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                               909
                                                                                                                                                                                                                                                                                                                                                                                                                    23-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                   04-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200100805-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB76594
                                                                                                                                           03
                                                                                                                                                                                                                                 27-AUG-1999
                                                                                            Pompejus
                                                                                                            (BADI )
                                                                     2001-071486/08.
DB; AAF67827.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mapping;
                                                                                                            BASF
                                                                                            ĭ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                            ĀG
                                                                                             Kroeger
                                                                                                                                                                                                                                                                                                                                                                                                                    2000WO-IB00926
                                                                                                                                                   99DE-1040831.
99DE-1040832.
99DE-1040833.
99DE-1041378.
99DE-1041379.
99DE-1041395.
99DE-1042077.
                                                                                                                                                                                                                                99DE-1033005.
99DE-1033006.
99DE-1040764.
                                                                                                                                    99DE-1042078
99DE-1042079
                                                                                                                                                                                                                 99DE-1040765.
99DE-1040766.
                                                                                                                                                                                                                                                        99DE-1032230
99DE-1032927
                                                                                                                                                                                                                                                                                                                                                                      99DE-1032122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genetic engineering.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                             æ
                                                                                            Schroeder H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID
                                                                                             Zelder
                                                                                            Ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NO:170
                                                                                             Haberhauer
```

Claim 20;

Page 404-406;

1119pp;

English

ç

AAF68080 encode the Corynebacterium glutamicum membrane

```
RESULT
AAB19774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Thes 7; Conserv
    Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
The present sequence is that of human protein tyrosine phosphatase HPTP-beta, a member of subclass III receptor type PTPs, bearing fibronectin type III-like repeats in the extracellular domain and a single catalytic domain in the cytoplasmic tail. HPTP-beta is a vascular-endothelial protein tyrosine phosphatase (VE-PTP) that specifically interacts with receptor-type tyrosine kinase Tie-2, modulating its tyrosine phosphorylation. Tie-2.1s involved in angiogenetic processes, the formation of blood vessels during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     construction and membrane transport (MCT) proteins given in AAB76510 to AAB76847. The MCT nucleic acids and proteins are useful in the identification of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria (e.g. Brevibacterium lactofermentum), the typing or identification of C. glutamicum or related bacteria, as reference points for mapping C. glutamicum genome, and as markers for transformation. AAF68082 and AAF68082 represent sequencing primers which are used in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB19774 standard; Protein; 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         example
                                                                                                                            Disclosure; Page 21-27;
                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                       (PLAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antimetastatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein tyrosine phosphatase; HPTP-beta; human; Tie-2; receptor-type tyrosine kinase; antiangiogenic; antitumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB19774;
                                                                                                                                                        tyrosine phosphatase
                                                                                                                                                                         g
                                                                                                                                                                                                                                WPI; 2000-648932/63
                                                                                                                                                                                                                                                          Fachinger G,
                                                                                                                                                                                                                                                                                                                    23-APR-1999;
                                                                                                                                                                                                                                                                                                                                               23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                             25-OCT-2000.
                                                                                                                                                                                                                                                                                                                                                                                                       EP1046715-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Domaín
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263 vqttpdfagqvt 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 IQTKPDRVGQAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                         regulating tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
                                                                                                                                                                                                                                                                                       MAX
                                                                                                                                                                                                                 AAA8866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from the present invention
                                                                                                                                                                         or modulating Tie-2 tyrosine kinase activity, useful e.g. ting tumor growth, using vascular-endothelial protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             913 AA;
                                                                                                                                                                                                                                                                                       PLANCK GES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                          Risau B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tyrosine phosphatase HPTP-beta
                                                                                                                                                                                                                                                                                                                    99EP-0108074
                                                                                                                                                                                                                                                                                                                                               99EP-0108074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1622..1641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "transmembrane domain"
1722..1967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52.8%;
                                                                                                                                                                    growth, using
                                                                                                                                                                                                                                                                                       FOERDERUNG WISSENSCHAFTEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                  "catalytic domain"
                                                                                                                           60pp;
                                                                                                                                                                                                                                                          Deutsch U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 38; DB 22;
Pred. No. 3.2e+02;
                                                                                                                            English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proteins given in AAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                       protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                       ø
```

```
RESULT
AAM78821
ID AAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local s
Matches 5
                                                                                                                                                                                                                                                                                  03-FEB-2000;
27-APR-2000;
20-JUN-2000;
19-JUL-2000;
The invention relates to polynucleotides (AAKS1456-AAKS3435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating cytokine, cell proliferation or cell differentiation or which may indu production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines peptide therapy. The polypeptides have various cytokine-like activitie e.g. stem cell growth factor activity, haematopoiesis regulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           embryonal development, wound healing and in pathological processes such as tumour development. VE-PTPs such as HPTP-beta or its catalytic domain, nucleic acids and ligands can be used to monitor, stimulate or repress Tie-2 activity for the purpose of monitoring or modulating angiogenesis, inducing or inhibiting vascular growth or remodelling and blood vessel maturation, and inhibiting tumour
                                                                                     Claim
                                                                                                                                                                                   Tang
Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1349
                                                                                                                   Nucleic
                                                                                                                                                                        Xue
                                                                                                                                                                                                                                                                        01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                       05-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                 WO200157190-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM78821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                  (HYSE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                    tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                               vaccine;
                                                                                                                                                                                                                                                  20-OCT-2000
                                                                                                                                                                                                                                                              5-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    \mathbf{L}
                                                                                                                                                                                  ζT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gsvrtkpdki 1358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GEIQTKPDRV
                                                                                                                                                    2001-476283/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or
C
                                                                                                                                                                                                                                                                                                                                                                                                                                   growth
                                                                                                      ending encoding polypeptides with cytokine-like activities in diagnosis and gene therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
5; Conserv
                                                                                                                                          AAK51954
                                                                                                                                                                                                                  HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                 Liu C,
Wang D,
                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide therapy; stem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1997
                                                                                                                                                                                                                                     2000US-0496914
2000US-0560875
2000US-0598075
2000US-0620325
2000US-0620325
2000US-063561
2000US-063325
2000US-0728422
                                                                                                                                                                                                                                                                                                                                       2001WO-US04098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                          factor; im
  disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ
                                                                                   3761-3764; 6221pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A
A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10
                                                                                                                                                                                 Drmanac I
Wang J,
                                                                                                                                                                        Wejhrman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NO 1483
                                                                                                                                                                                                                                                                                                                                                                                                                                   immunomodulatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .08;
                                                                                                                                                                       RT, Asundi V,
Zhang J, Ren
T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38; DB
Pred. No. 6.8e
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             cell
                                                                                   English
                                                                                                                                                                                                                                                                                                                                                                                                                                          growth factor; haemato;
                                                                                                                                                                                                                                                                                                                                                                                                                          inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and in pathological processes such as HPTP-beta or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 21;
6.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer; leukaemia;
                                                                                                                                                                                 zhou
F, C
                                                                                                                                                                                  Chen
                                                                                                                                                                                           ָס'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                 жх
ч
                                                                                                                                                                                                                                                                                                                                                                                                                                             haematopoiesis;
                                                                                                                                                                        ис,
`Wang
                                                                                                                                                                                  Cao Y,
ng ZW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
            activities,
                                                   elating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                        lating to 
7 induce
                                                                                                                                                                                           Ma
                                                                                                                                                                                            Υ,
                      or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
```

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSSSSSSS
                                                                                                                                                                                                                                                                                                                                                                                                                              AAM79805
                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                15-SEP-2000;
20-OCT-2000;
30-NOV-2000;
                                                                                                                                                                                                                  03-FEB-2000;
27-APR-2000;
20-JUN-2000;
19-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1349
                                                                                                                                        Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               activity, tissue growth factor activity, immunomodulatory activity activity/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis inflammation.
                                                                                                                                Хuе
                                                                                                                                                                                                                                                                                                                                                                                                                      AAM79805
                                                                                      Nucleic
                                                                                                                                                                 (HYSE-)
                                                                                                                                                                                                           01-SEP-2000;
                                                                                                                                                                                                                                                            05-FEB-2001;
                                                                                                                                                                                                                                                                            09-AUG-2001
                                                                                                                                                                                                                                                                                             WO200157190-A2
                                                                                                                                                                                                                                                                                                                             nervous
                                                                                                                                                                                                                                                                                                                                     tissue
                                                                                                                                                                                                                                                                                                                                              vaccine;
                                                                                                                                                                                                                                                                                                                                                                                      06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        were missing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: Records for SEQ ID NO 2110 (AAK52581), (AAM80020) are omitted as the relevant pages
                                                                                                                                                                                                                                                                                                                                                                                                                                       11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GEIQTKPDRV
                                                                                                                                ĄJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              gsvrtkpdki 1358
                                                                                                        2001-476283,
DB; AAK52938
                                                                                                                                                                                                                                                                                                                                                                     protein
                                                                                                                                                                                                                                                                                                                                 e; peptide therapy; stem cell growth factor; haematopoiesis; growth factor; immunomodulatory; cancer. lawkers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity
5; Conserv
                                                                             eacids encoding polypeptides with cytokine-like activities, in diagnosis and gene therapy -
                                                                                                                                                                 HYSEQ
                                                                                                                              Liu C,
Wang D,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1997 AA;
                                                                                                                                                                                2000US-0560875.
2000US-0598075.
2000US-0620325.
2000US-0654936.
2000US-0663561.
2000US-0693325.
2000US-0728422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                             2001WO-US04098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        at the time of publication
                                                                                                                                                                                                                                            2000US-0496914
                                                                                                                                                                 INC
                                                                                                                                                                                                                                                                                                                             disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10
                                                                                                                               Wang J,
Wejhrman
                                                                                                                                        Drmanac
Wang J,
                                                                                                                                                                                                                                                                                                                                                                     ij
                                                                                                                                                                                                                                                                                                                                                                                                                       Protein;
                                                                                                                                                                                                                                                                                                                                                                      Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50
                                                                                                                                                                                                                                                                                                                           immunomodulatory; cancer; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . 0%;
                                                                                                                                                                                                                                                                                                                                                                      3451.
                                                                                                                                 RT, Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                       2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 38; DB
Pred. No. 6.8e
4; Mismatches
                                                                                                                               Asundi V, and J, Ren Boodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22;
6.8e+02;
                                                                                                                                       Zhou P,
F, Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2111
from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AAK52582) and the sequence li
                                                                                                                                         7 ×
                                                                                                                                  u C,
Wang
                                                                                                                                                Cao
                                                                                                                                                                                                                                                                                                                                                    gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                listing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3666
                                                                                                                                                Ma
                                                                                                                                                ĸ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
```

cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating

Claim

20;

340-341; 6221pp;

English.

polypeptides (AAM78323-AAM80302)

that exhibit

(AAK51456-AAK53435) and that exhibit activity e

elating

ating to

9

useful

밁 S

0

```
RESULT
AAG92485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Tatches 5; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-DEC-1999;
07-APR-2000;
03-AUG-2000;
amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                   The present invention provides a number of the present invention provides a present invention. These sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nakagawa
Tateishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1354 gsvrtkpdki 1363
                                                                                                                                                                                                                                                                                                                                                                                                                  Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG92485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                               The present invention provides a number of nucleotide and protein
                                                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-DEC-2000; 2000EP-0127688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP1108790-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Coryneform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: Records for SEQ ID NO 2110 (AAKS2581), 2111 (AAKS2582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glutamicum protein fragment SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GEIQTKPDRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-376931/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 orm bacterium;
acid synthesi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            zκ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
                                                                                                                                                                                                                                                                                                                                                SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; 99JP-0377484.
; 2000JP-0159162.
; 2000JP-0280988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mizoguchi H,
                                                                                                                                                                                                                                                                                                                                                IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 накко косуо
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10
                                                                                                                                                                                                                                                                                                                                                NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein; 2993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52.8%;
50.0%;
                                                                                                                                                                                                                                                                                                                                             6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ikeda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ando
eda M,
                                                                                                                                                                                                                                                                                                                                             246pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 38; DB 22; Pred. No. 6.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S, Hayashi M,
Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ħ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ochiai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yokoi H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                     These
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
```

```
Sox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
                                                     Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, concernant of the central concernant of central concernant of the central concernant concernant concernant concernant concernant concernant central concernant concernant concernant concernant concernant central concernant concernant concernant concernant concernant central concernant central concernant concernant concernant concernant concernant con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU46616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
diagnostic agents for uncommentally (ELISA).
enzyme linked immunosorbent assay (ELISA).
enzyme linked immunosorbent assay (ELISA).
note: The sequence data for this patent did not form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Propionibacterium acnes vaccinating against and treating acne vulgaris .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :|| || || |
2343 vqttpdfagqvt 2354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-APR-2000; 2000US-199047P.
02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAPHO syndrome;
uveitis; endophi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU46616 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Propionibacterium acnes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Propionibacterium acnes immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-616774/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L'maisonneuve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-APR-2001; 2001WO-US12865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200181581-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 IQTKPDRVGQAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 58. 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ndrome; synovitis; acne; endophthalmitis; bone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID No 7811; 1069pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Persing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lesion; acne vulgaris;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      osteopathic; neuroprotectant. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ing DH,
Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptides and nucleic acids useful diagnosing infections, especially usef
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ĸ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mitcham JL, Wang S, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 38; DB 22
Pred. No. 1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pustulosis; hypertosis; osteomyelitis; joint; central nervous system; ELISA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ĀĀ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein #7512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               enzyme linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 especially useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunosorbent assay;
    part of the printed directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                   immunogenic
are used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
```

```
RESULT 1
AAUG2661
ID AAUG2661
AC AAUG
XX AAUG
XX SAPP
DE Prop
KW LIVE
KW LIVE
KW LIVE
PD 01-1
XX PO 01-1
XX 21-2
PR 02--
YX 21-2
PR 02--
YX XX 21-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SXS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                              pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-APR-2000;
02-JUN-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                          Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Propionibacterium acnes vaccinating against and treating acne vulgaris -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       at
                             enzyme linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; SEQ ID No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L'maisonneuve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200181581-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Propionibacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Propionibacterium acnes immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU62661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU62661 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pdrvgqa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-616774/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDRVGQA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 100 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; 2000US-199047P.
; 2000US-208841P.
; 2000US-216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Persing DH, Mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001WO-US12865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acnes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptides and nucleic acids useful for diagnosing infections, especially useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mitcham J
, Jen S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 37; DB Pred. No. 67; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JL, Wang
, Carter [
                             (ELISA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein #23557
     did
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ss,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 122;
     form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
part
     of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
```

```
RESULT
AAG90023
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                          16-DEC-1999;
07-APR-2000;
.03-AUG-2000;
                                                                                                                                                                                                                                                                                                               Nakagawa
Tateishi
                                                                  analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described
                                                                                                                                                                                                                                                                             WPI; 200
N-PSDB;
                                                                                                                                        The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. Tare useful for identifying the mutation point of a gene derived from
                                                                                                                                                                                                                           Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               specification, but was obtained in electronic
at ftp.wipo.int/pub/published_pct_sequences.
                                   Note: The sequence data for this specification, but was obtained
                                            particularly L-lysine. The present sequence in the exemplification of the invention. Note: The sequence data for this patent did
                                                                                                                             mutant of coryneform bacterium, measuring expression amount and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG90023
                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                          18-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP1108790-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAG90023;
                                                                                                                                                                                                                                                                                                                                                   (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 elevepqrvgq 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ν
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EIQTKPDRVGQ
                                                                                                                                                                                                                                                                             2001-376931/40.
B; AAH65242.
                                                                                                                                                                                            17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acid
                                                                                                                                                                                                                                                                                                                'nά
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; Protein;
                       Patent Office
                                                                                                                                                                                            SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144 AA
                                                                                                                                                                                                                                                                                                                                                                          99JP-0377484.
2000JP-0159162.
2000JP-0280988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          2000EP-0127688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         synthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
                                                                                                                                                                                                                                                                                                               Mizoguchi H, Ando
Senoh A, Ikeda M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first
                                                                                                                                                                                            ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino
                                                                                                                                                                                          246pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ
                                   ij
                                                                                                                                                                                                                                                                                                                S, Hayashi M,
Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 37;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ID NO:
                                   electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3777.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22;
                                not form part of the printed ic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                             Ochiai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                              Yokoi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WIPO
                                                                                                                                            Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
```

Query Match

51

48;

Score

37;

DB

22;

Length 250;

Sequence

Best Local Similarity 54.5%; Pred. No. 1.3e+02; Matches 6; Conservative 2; Mismatches 3; Indels

0; Gaps

0;

1 GEIQTKPDRVG 11 ||::|| | | 128 gevettptrag 138

Search completed: June 10, 2002, 15:21:06 Job time: 166 sec

```
Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OM protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched
      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
                                                                                                                                                          36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
  US-09-647-522-1
72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 June 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          283138 seqs, 96089334 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GEIQTKPDRVGQAT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000000000
                                                                                                                                                                                                                                                                                                                                      1360
1997
                                       214
241
304
311
339
339
500
601
151
151
116
192
293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2002, 15:19:00 ; Search time 35.61 Seconds (without alignments) 37.777 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DΒ
AH0502

BH12502

S76518

F69093

AE21699

T06699

T06699

T06699

T070609

S12050

B69350

T59406

AD1029

AB43021

F6456

AD1029

AB43021

AB43021

F6456

AD1029

AB43021

AB4302

AB4302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JC7371
T14578
T28872
JC4747
S32482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                            hypothetical prote probable membrane hypothetical prote aliphatic amidase aliphatic amidase
                                                     probable mitochond probable membrane o-pyrocatechuate d
                                                                                                                                  probable membrane
transposase (clone
hypothetical prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           toxin - jellyfish
nucleoporin Nup153
hypothetical prote
                  hypothetical
hypothetical
                                                                                                               ribosomal protein
                                                                                                                                                                                             RNA-directed RNA p
                                                                                                                                                                                                                                                                                              hypothetical
hypothetical
                                                                                                                                                                                                                                                                                                                                    protein-tyrosine-p
                                                                                                                                                                                                                                                                                                                                                      cation transport A zinc finger protei
                                                                                                                                                                                                                                                                                                                                                                                                RNase L inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          electron transfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            adenylate cyclase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                                                                                                                                                                                 probable ATP/GTP-b
                                                                                                                                                                                                                                                                                                                                                                                                                                                       transaldolase B [i
                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical
  hydrolase
                prote
                                                                                                                                                                                                                                                                                                               prote
                                                                                                                                                                                                                                                                                                                                                                                                                prote
```

A;Cross-references: A;Accession: PC7094 A; Molecule type: mRNA A; Residues: 1-450 < NAG>

DDBJ:AB015878

ALIGNMENTS

C;Accession: JC7371; PC7094
R;Nagai, H.; Takuwa, K.; Nakao, M.; Ito, E.; Miyake, M.; Noda, M.; Nakajima, T.
Biochem. Biophys. Res. Commun. 275, 582-588, 2000
A;Title: Novel proteinaceous toxins from the box jellyfish (sea wasp) Carybdea raston A;Reference number: JC7371
A;Accession: JC7371
A;Accession: JC7371

toxin - jellyfish (Carybdea raston1)
c;Species: Carybdea raston1
c;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 17-Nov-2000

jellyfish (Carybdea rastoni)

```
nucleoporin Nup153 homolog - African clawed frog (fragment)
c;Speciles: Xenopus laevis (African clawed frog)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000
C;Accession: T14578
R;Shah, S.; Tugendreich, S.; Forbes, D.J.
J. Cell Biol. 141, 31-49, 1998
A;Title: Major binding sites for the nuclear import receptor are the internal nucleop
A;Reference number: Z18147; MUID:98198465
                                                                                                                                                                                                                                                                                                                                                           RESULT
T14578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein A; Residues: 39-55;56-70;196-210;250-267;268-279;309-325;363-377;378-382 <NA2>C; Comment: This protein, a member of bioactive protein, has hemolytic activity C; Keywords: hemolysis; inflammation; toxin
                                                                                                  A; Cross-references:
                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNA
A;Residues: 1-1219 <SHA>
                                                                                                                                                                          A; Reference number: A; Accession: T14578
                                                                                                                                                                                                                                                                                                                                                                                                                                        В
Query Match
Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                        56 GEIQTKPDRVGQAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GEIQTKPDRVGQAT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
14; Conserv
    Similarity
8; Conser
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                            EMBL:AF045567; NID:g3047239; PID:g3047240; PIDN:AAC41273
                                                                                                                                                                                                                                                                                                                                                                                                                                        69
                    61.1%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
Score 44; DB
Pred. No. 11;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 72; DB 2;
Pred. No. 2.2e-05;
Mismatches 0;
                                     2:
                                  Length 1219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 450;
  Indels
  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activity
  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
```

δõ

1 GEIQTKPDRVGQAT 14

```
F;873-895/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;893-919/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;943-964/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;1007-1029/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;1259-1282/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;1283-1306/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;1283-1306/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;1748-1991/Domain: catalytic #status predicted <CAT>
F;1769-1854/Domain: yeast adenylate cyclase catalytic domain homology <YACC>
F;1994-1999,2125-2129/Domain: CAP-binding #status predicted <CAP>
F;2035-2063/Region: leucine zipper motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Reference number: Z20535
A;Accession: T28877
A;Stafin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Miller, N.
submitted to the EMBL Data Library, Decemposition. The sequence of C. elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              adenylate cyclase (EC 4.6.1.1) - Podospora anserina N;Alternate names: 3'5'-Cyclic AMP synthetase; adenyl cyclase; C;Species; Podospora anserina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-2145 <LOU>
A;Cross-references: GB:L43413; NID:g1261824; PIDN:AAB05642.1; PID:g1480208
A;Crosment: This protein is produced by a mutation in a vegetative incompatibility-contro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 21-Jul-2000
C;Accession: JC4747
R;Loubradou, G.; Begueret, J.; Turcq, B.
                                                                                                                                                                                                                                                                                                                        F;826-849/Domain:
F;850-872/Domain:
                                                                                                                                                                                                                                                                                                                                                                    F;694-1372/Domain: leucine-rich #status predicted <LEU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: JC4747; A; Accession: JC4747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: An additional copy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position: X
A; Introns: 216/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-997 <MIL>
A; Residues: 1-997 <MIL>
A; Cross-references: EMBL:U41538; PIDN:AAC48181.1; GSPDB:GN00028; A; Cross-references: Strain Bristol N2; clone R04E5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Introns:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ypothetical protein R04E5.8 - Caenorhabditis elegans; Species: Caenorhabditis elegans; Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #to; Accession: T28872
                                                                                                                                                                                                                                                                                                                                                                                            ;Keywords: leucine zipper; phosphorus-oxygen lyase
                                                                                                                                                                                                                                                                                                                                                                                                                  ;Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genetics:
                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 985
    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PaAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CESP: R04E5.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EARPDRIGQA 994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QTKPDRVGQA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119-123,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSAQTKPDTLSQST
                                                                                                                                                                                                                                                                                                                                                                                                                                       79/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
6; Conserv
  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                               yeast adenylate cyclase; leucine-rich alpha-2-glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                          319/3; 2091/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Begueret, J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234/3;
                                                                                                                                                                                                                                                                                              leucine-rich alpha-2-glycoprotein repeat
leucine-rich alpha-2-glycoprotein repeat
                                                                                                                                                                                                                                                                                                                                              leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         255/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55.6%;
55.6%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the adenylate MUID:96200867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            305/1; 669/3; 891/1; 986/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40;
Pred. No.
  Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       December 1995
  40;
No:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cosmid R04E5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
47;
  DB 2;
1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cyclase-encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 997
                        Length 2145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                           homology <LRR2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene relieves developmenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           adenylylcyclase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                      homolog
                                             δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
    DЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
```

267

1 GEIQTKPDRVGQA

```
In.
S.; Moule, S.; O'vacar.
Nature 413, 848-852, 2001
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, A;Authors: Complete genome sequence of a multi-A;Reference number: AB0502; PMID:11677608
**Accession: AH0502
                                                                                    A; Gene: STY0007
C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                               A; Note: this species has also been call
C; Date: 09-Nov-2001 #sequence_revision
C; Accession: AH0502
                                                                                                                                                                                                                                                                                                                                                                                                  transaldolase B [imported] - Salmonella enterica subsp. enter
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Superfami
C; Keywords:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GDB:119887;
A;Map position: 19q13.4-19q13.4
C;Complex: heterodimer of alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Finocchiaro, G.; Colombo, I.; Garavaglia, B.; Géllera, C.; Valdameri, G.; Eur. J. Biochem. 213, 1003-1008, 1993
A;Title: cDNA cloning and mitochondrial import of the beta-subunit of the hua;Reference number: S32482; MUID:93279298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Description: electron transfer from any of several dehydrogenases in the mitochondr C;Superfamily: electron transfer flavoprotein beta chain C;Keywords: electron transfer; FAD; flavoprotein; heterodimer; mitochondrial matrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X71129; C;Comment: This protein does not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               electron transfer
                                                                                                                                            A; Cross-references:
                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-317 <P
                                                                                                                                                                                                                                                                                                                                                  R;Parkhill,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: GDB:ETFB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-255 <FIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;Accession: S32482
                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                  T.; Connerton, F., C.
S.; O'Gaora,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 EIQTKPDRVGQAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ഗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KIRVKPDRTGVVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IQSLPDNVGQMT 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IQTKPDRVGQAT
                                                                                                                                                                                                                                                                                                           J.; Dougan, G.; James, K.D.; nerton, P.; Cronin, A.; Davis, S.; O'Gaora, P.
Similarity
5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S32482
                                                                                        human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
 Conservative
                                                                                                                                                             <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               flavoprotein beta chain -
                                                                                                                                            GB:AL513382; PIDN:CAD01160.1;
                                                                                        transaldolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14
                 38.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52.8%;
                                                                                                                                                                                                                              quence of a multiple drug resistant Salmonella enterica PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (see PIR:A31998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OMIM: 130410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NID:g297901; PIDN:CAA50441.1; have a cleavable transit pept:
 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 38; DB Pred. No. 26; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>,</u>
                 Score 38;
Pred. No.
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-Jul-1996 #text_change 11-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                      09-Nov-2001 #text_change
                                                                                                                                                                                                                                                                                                                               Thomson, N.R.; Pickard, P.; Davies, R.M.; Dowd
               DB
33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human
                                  2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ۲.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and beta chains that binds one molec
                                                                                                                                            PID:g16501290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  r:cAA5U441.1; PID:g297902
transit peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ω
-:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     beta-subunit of the human elect
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          enterica serovar Typhi
                                                                                                                                                                                                                                                                                                                                Dowd,
                                                                                                                                              GSPDB:GN00176
                                                                                                                                                                                                                                                                                                                               D.; Wain, J.; Church
, L.; White, N.; Farr
                                                                                                                                                                                                                                                                                                                                                                                        27 - Nov - 2001
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Garbuglio
 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                            (strai
                                                                                                                                                                                                                                                         se
```

```
hypothetical protein - Syn
C.Species: Synechocystls s
A; Variety: PCC 6803
C.Date: 25 Apr.1997 #seque
C; Accession: S76518
R; Kaneko, T.; Sato, S.; Ko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Kocessau...
A; Status: preliminary
A; Molecule type: DNA
A; Molecule: 1-368 < PAR>
A; Residues: 1-368 < PAR>
A; Cross-references: GB: AL139079;
A; Cross-remental source: serotype (
             RNase L inhibitor - Methanobacterium thermoautotrophicum (;Species: Methanobacterium thermoautotrophicum C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_C;Accession: F69093
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee,
                                                                                                                                                                                                                                                                                                                                                                                                                                            O, K.; O)
DNA Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable ATP/GTP-binding protein (mrp protein homolog) Cj1606c (imported] - C;Species: Campylobacter jejuni c;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Sep-2000 C;Accession: D81256 R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher. C . Rasham
                                                                                        RESULT
F69093
                                                                                                                                                                                                                                                                                                                                      A; Reference number: $74322;
A; Accession: $76518
A; Status: nucleic acid seque
A; Molecule type: DNA
A; Residues: 1-476 <KAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
S76518
                                                                                                                                                밁
                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: mrp; C; C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: The genome sequence A;Reference number: A81250; MA;Accession: D81256
                                                                                                                                                                                                                                                                                                                            A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 403,
                                                                                                                                                                                                                                                                                A;Start
                                                                                                                                                                                                                                                                                                            A; Note: the nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C.W.; Quail,
   Qiu,
                                                                                                                                                                                                                                                                                                                                                                                                                                          K.; Okumura, S.; S
WA Res. 3, 109-136,
                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
   D.;
                                                                                                                                                440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146
                                                                                                                                                                            1 GEIQTKP--DRVGQAT 14
                                                                                                                                                                                                                                                                                codon:
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GEIQTKPDRVGQ
                                                                                                                                                GEVRFLPNGDRAGQAT 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GETKTQPEVVGQ
   Spadafora,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J.; Wren, B.W.; Mungall, l, M.; Rajandream, M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                665-668,
                                                                                                                                                                                                         Similarity
9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cj1606c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 7; Conserv
   Doucette-Stamm,
dafora, R.; Vica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            analysis of the genome
                                                                                                                                                                                                                                                                                                                                                                    acid sequence not shown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      S.; Kotani, H.; Tanaka, A.; Asamizu, Shimpo, S.; Takeuchi, C.; Wada, T.; V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                            EMBL:D64002;
lde sequence v
                                                                                                                                                                                                                                                                                                                                                                                                                                             1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synechocystis sp. (strain PCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable
                                                                                                                                                                                                                     56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.8%;
 Vicaire,
                                                                                                                                                                                                                                                                                                                                                                                               MUID:97061201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the food-borne pathogen Campylobacter jejuni reveals MUID:20150912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GB:AL111168; NO O2, strain NCTC
                                                                                                                                                                                                                                                                                                            GB:AB001339; was submitted
                                                                                                                                                                                                       Score 38; DB
Pred. No. 50;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ω
                                                                                                                                                                                                         2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 38; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   membrane
   æ
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rutherford, K.M.;
 Deloughery,
.; Wang, Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
Wang,
                                                                                                                                                                                                                                                                                                                                                                                                                            of the
                                                                                                                                                                                                                  DB
50;
                                                                                                                                                                                                                                                                                                                                                                  translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NID:g6968971; PIDN:CAB73594.1; PID:g69690:
TC 11168
                                                                                                                                                                                                                                                                                                          NID:g1001612; PIDN:BAA10364.1; to the EMBL Data Library, June
                                                                                                                                                                                                                                    2
                                                                                                                                                                                                                                                                                                                                                                                                                            unicellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
 C.; Lee, H.;
Wierzbowski,
                                          #text_change 02-Feb-2001
                                                                                                                                                                                                       Ψ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YIL003w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2
                                                                                                                                                                                                                                 Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Churcher,
VanVliet, A
                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                    not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Watanabe,
                                                                      (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E.; Nakamura,
                                                                                                                                                                                                                                                                                                                                                                                                                            cyanobacterium
Dubois, J.;
J.; Gibson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Α.;
                                                                       Delta
                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A
:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Basham, D.; Chillin
Whitehead, S.; Barre
                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
               ٦
;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yamada,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ۲.,
                                                                      Ξ
Aldredge, T
R.; Jiwani,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        міуајіma,
da, м.; Yas
                                                                                                                                                                                                                                                                                                                                                                                                                           Synechocysti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Campylobact
                                                                                                                                                                                                                                                                                                            PID:d10110
1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yasud
 ), T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               γţ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
AE2169
                                                                                                                                                                                                       밁
                                                                                                                                                                                                                               QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                               T06699
```

```
A; Experimental C; Genetics:
A; Gene: all2908
zinc finger protein T29H11.50 - Arabidopsis thaliana
c;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change
C;Accession: T06699
R;Quetler, F.; Choisne, N.; Robert, C.; Brottler, P.; Wincker, P
submitted to the Protein Sequence Database, April 1999
A;Reference number: 215793
A;Accession: T06699
A;Residues: 1-1360 <QUE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C:Superfamily: ribonuclease L inhibitor; ATP-binding co:Keywords: ATP; nucleotide binding; P-loop F;37-101/Domain: ferredoxin 2[4Fe-4S] homology <FER2>F;119-318/Domain: ATP-binding cassette homology <ABC1>F;137-114/Region: nucleotide-binding motif A (P-loop) F;337-114/Region: nucleotide-binding motif A (P-loop) F;386-561/Domain: ATP-binding cassette homology <ABC2>F;403-410/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Acession: AE2169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: C; Genetics: A; Gene: MTH1695
                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-735 <KUR>
A;Cross-references: GB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: AE2169
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cation transport ATPase all2908 [imported] - C;SpecLes: Anabaena sp. (strain PCC 7120) is a s A;Note: Anabaena sp. (strain PCC 7120) is a s C;Date: 14-Dec-2001 #sequence_revision 14-Dec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-623 <MTH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary; nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: F69093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Complete genome sequence of Methanobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nakazaki, N.;
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S.; Church, G.M.; Daniels, C.J
Bacteriol. 179, 7135-7155, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             356
                                                                                                                                                                                                                                   297
                                                                                                                                                                                    11
                                                                                                                                                                                                                                                                1 GEIQTKPDRVGQAT
                                                                                                                                                                                                                                                                                                                                                                                    a112908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 EIQTKPDRVGQA
                                                                                                                                                                                                                                GEIYIQAERVGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EFKVKPPRVGEA
                                                                                                                                                                                                                                                                                                 Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shimpo,
                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  GB:BA000019; PIDN:BAB74607.
ce: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GB:AE000927; GB:AE000666; ce: strain Delta H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A69000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (strain PCC 7120) is a synonym of Nostoc sp. strain PC
sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13
                                                                                                                                                                                                                                                                  14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .; Sugimoto, M.; Takazawa, M.;
                                                                                                                                                                                                                                   310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.8%;
58.3%;
                                                                                                                                                                                                                                                                                                                   52
57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MUID:98037514
                                                                                                                                                                                                                                                                                                                   C.J.; Mao,
                                                                                                                                                                                                                                                                                                  2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 38; DB
Pred. No. 67;
2; Mismatches
                                                                                                                                                                                                                                                                                                                Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2:
                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                  38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kuritz, T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ٠
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
67;
                                                                                                                                                                                                                                                                                                                   DB
81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anabaena sp. (strain PCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NID: g2622822;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rice,
                                                                                                                                                                                                                                                                                                                                                                                                                                  .
H:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        shown;
                                                                                                                                                                                                                                                                                                                                                                                                                                PID:g17132002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ω
                                                                                                                                                                                                                                                                                                                                 Length 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sasamoto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P.; Noelling, J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cassette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thermoautotrophicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamada,
                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIDN: AAB86167.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             s.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        homology;
                                                                                   ۳
:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :
:
                                                                                                                 22-Oct-1999
                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                  GSPDB:GN00179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Watanabe,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              strain PCC
                                                                                   Cattolico,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yasuda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          not
                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cyanobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reeve,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P
                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ٠
.
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PID: 9262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                   ۲
:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Irigu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ξ:
                                                                                   Art
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fu
```

```
RESULT
B69350
                                                                                                                                                                                                                                                                                                                                                                                                              C:Superfamily: protein-tyrosine-phosphatase, receptor type beta; fibronectin type (Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; F:1-22/Domain: signal sequence #status predicted <SIG>F:23-1997/Product: protein-tyrosine-phosphatase, receptor type beta #status predicted <F:23-1625/Domain: extracellular #status predicted <EXT>
                                                                                                                                                                                                                                                                                                    F;1626-1642/Domain: transmembrane *status predicted <TMN>F;1643-1997/Domain: intracellular *status predicted <IMT>F;1727-1952/Domain: protein-tyrosine-phosphatase homology <PTP>F;1904/Active site: Cys (phosphocysteine intermediate) *status predicted F;1910/Binding site: substrate phosphate (Arg) *status predicted
                                                                                                                                                    δÕ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-1997 < KRU>
A;Cross-references: GB:X54131; NID:g35787; PIDN:CAA38066.1; PID:g35788
A;Cross-references: GB:X54131; NID:g35787; PIDN:CAA38066.1; PID:g35788
R;de'Vries, L.; Li, R.Y.; Ragab, A.; Ragab-Thomas, J.M.F.; Chap, H.
FEBS Lett. 282, 285-288, 1991
A;Title: Expression of a truncated protein-tyrosine phosphatase mRNA in A;Reference number: S15818; MUID:91243813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S12050; S15818; S15819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: 3
A;Introns: 294/1; 320/2;
C;Keywords: P-loop; zinc
  hypothetical
                                                                                                             Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross · references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: Structural diversity and evolution of A; Reference number: $12049; MUID:91006018 A; Accession: $12050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Krueger, N.X.; Streuli, M.; Saito, H. EMBO J. 9, 3241-3252, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type beta precursor - human C; Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: ATSP:T29H11.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:AL049659; GSPDB:GN00061; ATSP:T29H11.50
A;Experimental source: cultivar Columbia; BAC clone T29H11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position: 12q15-12q21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: GDB:PTPRB; PTPB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1872-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: not compared with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: S15819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1872-1911, 'VHMVLQK'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type:
A; Residues: 1-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: S15818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genetics:
                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                             1349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1195 GSLETKPKKIGK 1206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                              13
                                                                                                                                                      1 GEIQTKPDRV 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GEIQTKPDRVGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      not compared with conceptual translation
                                                                                                             GSVRTKPDKI 1358
protein AF0802 -
                                                                                                                                                                                                Similarity
5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 41.7
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA
                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GDB:127352; OMIM:176882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <VR2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  343/1; 393/2; 601/1; 765/1; 892/3
                                                                                                                                                                                                                     52.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52,8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conceptual translation
  Archaeoglobus fulgidus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <VRI>
                                                                                                                                                                                                4
                                                                                                                                                                                                Score 38; DB Pred. No. 2.464; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 38; DB
Pred. No. 1.66
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; DB 2; 1
1.6e+02;
                                                                                                                                                                                                                                       DB
                                                                                                                                                                                         .4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human receptor-like protein tyrosine
                                                                                                                                                                                                                                     Length 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1360;
                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      beta #status predicted
                                                                                                                                                                                                                                                                                                                             predicted
                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human
                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  recept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    III re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phos
                                                                                                                                                                                                                                                                                                                                                                                                                                        ş
                                                                                                                                                                    C;Species: Salmonella enterica subsp. enterica serovar Typha;Note: this species has also been called Salmonella typhic;Date: 09-Nov-2001 *sequence_revision 09-Nov-2001 *text_c;Date: 09-Nov-2001 *sequence_revision 09-Nov-2001 *c;Accession: AD1029
R;Parkhill, J; Dougan, G; James, K.D; Thomson, N.R.; Pi
                                                       Nature 413, 848-852, 2001
A; Authors: Parry, C.; Quail, M.; R
A; Title: Complete genome sequence
                                                                                                                                                                                                                                                               probable membrane protein STY4557 [imported] - C; Species: Salmonella antorio
                                                                                                                                                                                                                                                                                                        RESULT
AD1029
                  A; Reference number: AB0502; A; Accession: AD1029
                                                                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession:
R; Klenk, H.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                 Connerton, F.,
Connerton, F.,
S: O'Gaora,
```

P.; Cronin, A.;

Davis,

Thomson, N.R, P.; Davies,

æ

Pickard, R.M.; Dowd,

D.; 1

; Wain, J

J.; Church e, N.; Farr

orted] - Salmonella enterica subsp. enterica serovar Typhi

enterica

se

09-Nov-2001 #text_change

09-Nov-200

, M.; Rutherford, K.; Simmonds, M.; quence of a multiple drug resistant PMID:11677608

Skelton, J Salmonella

enterica se

```
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch A;Reference number: A69250; MUID:98049343
A;Status: prolimination of the hyperthermophilic, sulfate-reducing arch A;Status: prolimination: B69350
A;Status: prolimination: MUID:98049343
                                                                                                                                                                                                                                                     A;Cross-references: EMBL:AL137099; PIDN:CAB68658.1; A;Experimental source: strain 972h(-); clone pl p463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE001049; GB:AE000782; C;Superfamily: hypothetical protein AF0802
                                                                                                                                                                                         A; Map position:
                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary; translated from
                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: A; Accession: T50406
                                                                                                                                                                                                                                                                                                                                                                                                          R;Rieger, M.; McDougall, R.C.; Rajandream, M.A.;
submitted to the EMBL Data Library, January 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: T50406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Schizosaccharomyces pombe
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein SPBP4G3.03 [imported] - fission yeast (Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-214 <KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; nucleic acid sequence not shown;
                                                                                                                                                                                                                                                                                                      Residues: 1-241 <RIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Date: 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Species: Archaeoglobus fulgidus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fleischmann, R.D.; Quackenbush, J.;
91 GQIETKPD 98
                                   1 GEIQTKPD 8
                                                                                                  Local Similarity
                                                                                                                                                                                                                 SPDB:SPBP4G3.03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GEIQTKPDRVG 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; chmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GELEEQPDKLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B69350
                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                          Z25068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90
                                                                                                    51.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51.48;
45.58;
                                                                                                    Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                              GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NID:g2689372; PIDN:AAB90445.1; PID:g264
                                                                                                                          2
                                                                                                                                                                                                                                                                                                                                                                                                                                Barrell, B.
                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #text_change
                                                                                                                          Length 241;
                                                                                                                                                                                                                                                                                  GSPDB:GN00067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 214;
                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E.; Ketchum, K.A.; Dod
Gill, S.; Kirkness, E
                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                  SPDB:SPBP4G3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kirkness,
                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pombe
```

P26009 014157 024742 P76616 P10788 P38526

5 saccharomyc 9 gallus gall 7 schizosacch 2 drosophila 6 escherichia 8 haloarcula 6 thermotoga

Oynr64 homo sapien P20945 emericella O54443 streptococc P35220 drosophila P22515 gazzati

Q9nr64 P20945 Q54443

```
Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                         Pred. No. is the number of results predicted by chance to have a and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB seq length: 0
DB seq length: 2000000000
                                                                                                                                                                            50.0
50.0
50.0
50.0
50.0
48.6
48.6
48.6
48.6
48.6
48.6
48.6
                                                                                                                              47
47
47
47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.6
52.8
52.8
52.8
51.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein search, using sw model
                                                                                340
455
1816
2748
395
486
486
584
630
641
658
700
807
4488
700
807
4488
1160
357
398
415
398
447
447
447
447
522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SwissProt_40:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105224 seqs, 38719550 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             June 10, 2002, 15:21:45; Search time 18'65 Seconds (without alignments) 29.066 Million cell upr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GEIQTKPDRVGQAT 14
                                                                                                                                                                                                                                                                                                                                                                                                                        2145
255
773
1997
311
443
500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyright (c) 1993 - 2000 Compugen
                                                                                                           Y825_STRCO
HYEP_HUMAN
AF6_HUMAN
AF6_HUMAN
NUM1_YEAST
THB_PAROL
HYDH_ECOLI
RADA_MYCTU
YMB3_YEAST
GIDA_ESEPU
SUM_YEAST
GIDA_ESEPU
SUS1_HORNU
RSPA_CVMJH
RSTA_AQUAE
YCIL_HAEIN
KAPC_YEAST
BRNQ_LACDL
ZIC1_HUMAN
ZIC1_MOUSE
                                                                                  INVO_HYLLA
GIDA_COXBU
                                                                                                                                                                                                                                                                                                                                                                                                ETFB_HUMAN
YHGF_ECOLI
PTPB_HUMAN
MCH_HALN1
ZIC1_XENLA
RRPA_CVMJD
R18E_HALMA
                                                                                                                                                                                                                                                                                                                                                                                   DHBD_ASPNG
                                                                     Q15915
P46684
P17941
P94613
                                                                                                                                                                                        P39098 mus musculu
P15179 saccharomyc
P57938 pasteurella
P31922 hordeum vul
                                                                                                                                                              P19751
067690
P45104
                                                                                                                                                  P05986
                                                                                                                                                                                                                                                                                  p26627 murine care
p1273 haloarcula
p80346 aspergillus
p005954 streptomyce
p55196 homo sapien
p00402 saccharomyc
p14377 paralichthy
p35570 myccharitha
                                                                                                                                                                                                                                                                                                                                                                                                                           P38117 homo sapien
P46837 escherichia
P23467 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                073689 xenopus lae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 001513 podospora a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ltd
                                              5 homo sapien

4 mus musculu

1 hylobates 1

3 coxiella bu

7 rhizobium s
                                                                                                            5 saccharomyc
3 xylella fas
4 lactobacill
                                                                                                                                                  1 murine coro
0 aquifex aeo
4 haemophilus
                                                                                                                                                                                                                                            Pseudomonas
                                                                                                                                                                                                                                                        saccharomyc
                                                                                                                                                                                                                                                                       mycobacteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell updates/sec
                                   THE SECOND PROPERTY OF SECOND PR
         Pfam; PF00211; guanylate_cyc; 2.
Pfam; PF00260; LRR; 15.
Pfam; PF00481; PP2C; 1.
SMART; SM0019; LEURICHRPT.
SMART; SM00344; CYCC; 1.
SMART; SM00370; LRR; 5;
SMART; SM00370; LRR; 5;
SMART; SM00359; LRR, TYP; 1.
SMART; SM00359; P2CC; 1.
SMART; SM00332; PP2CC; 1.
PR051TP; PS50125; GUANYLATE_CYCLAS
PROSITE; PS50125; GUANYLATE_CYCLAS
REPEAT
REPEAT
751
776
LRR 1
                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation modified and this statement is not removed. There are no restrictions on its or send an email to license disease. Usage by and for commercial or send an email to license disease.
                                                                                                                                                                           InterPro; IPR000159;
                                                                                                                                                                                                Interpro; IPR001611; LRR.
Interpro; IPR003592; LRR.
Interpro; IPR003591; LRR.
                                                                                                                                                                                     Interpro; IPR001932;
                                                                                                                                                                                                                           EMBL; L43413; AAB05642.1; InterPro; IPR001054; Guanylt_cyclase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
CYAA_PC
                                                                                                                                                                                                                                                                                                                                                CAMP.

CATALYTIC ACTIVITY: ATP = 3',5'-CYClic AMP + dip-
-!- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-3
-!- SIMILARITY: CONTAINS 21 LEUCINE-RICH REPEATS (LE
                                                                                                                                                                                                                                                                                                                                                                                                               Loubradou G., Begueret J., Turcq B.;
An additional copy of the adenylate cyclase-encoding gene relieves incompatibility-controlling gene in Podospora anserina.",
Gene 170:119-123(1996).
I- FUNCTION: PLAYS ESSENTIAL ROLES IN REGULATION OF CELLULAR METABOLISM BY CATALYSING THE SYNTHESIS OF A SECOND MESSENGER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 01-NOV-1997 (Rel. 16-OCT-2001 (Rel. 1891)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96200867; PubMed=8621071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Podospora anserina.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
cordariales; Lasiosphaeriaceae; Podospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYAA_PODAN
Q01513;
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cyclase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adenylate cyclase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _PODAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34
35
36
37
38
39
40
41
42
                             GUANYLATE_CYCLASES_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LRR_typ.
PP2C_domain.
                                                                                                                                                                                                           LRR_out.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35, Created)
35, Last sequence update)
40, Last annotation update)
9 (EC 4.6.1.1) (ATP Pyrophosphate-lyase) (Adenylyl
repeat; самр synthesis; маgnesium.
LRR 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   748
796
850
935
1024
1044
2104
2104
2106
3828
110
128
155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KHL1_HUMAN
ABAA_EMENI
DEXT_STRMU
CTNA_DROME
UBA1_YEAST
ITAB_CHICK
MYS3_SCHICK
MYS3_SCHICK
MYS3_SCHICK
MYS3_SCHICK
MYS3_SCHICK
MYS3_SCHICK
MYS3_SCHICK
MYS3_SCHICK
MYS3_SCHICK
MYS3_CHICK
MYS3_CHICK
MYS3_CHICK
MYS3_CHICK
MYS3_CHICK
MYS3_CHICK
MYS3_CHICK
RS1_HALMA
RS7_HEMA
RS7_HEMA
RS7B_AQUAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
                                                                                                                                                                                                                                                                                                                                                                                  + diphosphate.
SS-3 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                          (LRR).
```

```
RESULT
ETFB_H
                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
                                                                                                                                                                                                                            P38117;
01-0CT-1994 (Rel. 3
01-0CT-1994 (Rel. 3
16-0CT-2001 (Rel. 4
Electron transfer f
                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                                                                                         LT 2
HUMAN
                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                  ETFB_HUMAN
                                                                                                                                                                                                                                                                                                      907
                                                                                                                                          TISSUB-Fetal liver;
MEDLINE-93279298; PubMed-8504797;
Finocchiaro G., Colombo I., Garav,
Garbuglio N., Didonato S.;
                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                      human electron-transfer flavoprotein.";
Eur. J. Blochem. 213:1003-1008(1993).
                                                                                                                                                                                                                                                                                                              3 IQTKPDRVGQAT
                                                                                                      X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
             Colombo I., Finocchiaro G., Garavaglia B., Garbuglio N., Yamaguchi S., Frerman F., Berra B., Didonato S., Yamaguchi S., Frerman F., Berra B., Didonato S., White and polymorphisms of the gene encoding the beta subunit the electron transfer flavoprotein in three patients with glutaric the electron transfer flavoprotein in three patients.
                                                                         "Three-dimensional structure to 2.1-A resolution.";
                                                                                       CDNA cloning and mitochondrial import
                                                                 Proc. Natl. Acad. Sci. U.S.A. 93:14355-14360(1996).
                                                   VARIANT GAILB GLN-164
      acidemia type II.";
                                                                                                                                                                                                                                                                                                      IQSLPDNVGQMT 918
                                                                                                                                                                                                                                                                                                                                    Similarity 66.1
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              1099
1233
1257
1257
1282
1305
1357
1357
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1028
1053
1075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        983
                                                                                                                                                                                                                                                                                                                                                                           A.
                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        917
940
965
1005
                                                                                                                                                                                                                                                                                                                                                                                                 1328
1380
1419
1710
                                                                                                                                                                                                                                                                                                                                                                                                                              1097
1120
1256
1280
1304
                                                                                                                                                                                                                                                                                                                        14
                                                                                                                                                                                                                                 30, Created)
30, Last sequence update)
40, Last annotation update)
flavoprotein beta-subunit (Beta-ETF)
    3:429-435(1994)
                                                                                                                                                                                                                                                                                                                                               55.6%;
                                                                                                                                                                                                                                                                                                                                                                             237515
                                                                                                                                                                                                                                                        Created)
                                                                                                                                                       I., Garavaglia B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LRR
LRR
LRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LRR
                                                                                                                                                                                                                                                                                                                                        Score 40; DB pred. No. 46; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRR
LRR
                                                                                                                                                                                                                                                                                                                                                                                             PP2C-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                           LRR 20
LRR 21
                                                                                                                                                                                                                                                                                                                                                                                                                                 LRR
LRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ĿRR
                                                                                                                                                                                                                                                                                                                                                                                      POLY-SER
                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10
11
13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         σ
                                                                                                                                                                                                                                                                                                                                                                              88E7EF6E4AC0687D CRC64;
                                                                                                                                                                                                                                                                          255
                                                                                                                                             of.
                                                                                                                                                                                                                                                                                                                                                            ۲,
                                                                                                                                             the beta-subunit of the
                                                                                                                                                            Gellera C.,
                                                                                                                                                                                                                                                                                                                                                            Length 2145;
                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                valdameri G
                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                  Gaps
                                      Of.
                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                       RESULT 3
YHGF_ECOLI S'
ID YHGF_ECOLI S'
AC 94687; P76689;
DT 01-NOV-1995 (Rel
DT 15-JUL-1999 (Rel
                                                                                 밁
                                                                                              Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bross P., Pedersen P.,
                                                                                                              Matches
                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                      -
                                                                                                                                                                                                                                     PIR; $32482; $3245;
PDB; 1EFV; 03-DEC-97.
MIM; 130410;
                                                                                                                                                    SEQUENCE
                                                                                                                                                                 VARIANT
                                                                                                                                                                                 VARIANT
                                                                                   19
                                                                                          2 EIQTKPDRVGQAT 14
:|: |||| |
                                                                                                                                                                                                                                                    S32482;
                                                                                   KIRVKPDRTGVVT
                                                                                                                Similarity
7; Conserv
                                                                                                                                                                                                                                                       S32482
                                                                                                                                                       255
                                                                                                                                                                    164
                         (Rel.
                                                                                                                  Conservative
                                                                                                                                                        AA;
                                                STANDARD;
                            32, Created)
38, Last sequence
                                                                                       31
```

δÃ

밁

Genet.

Created)

update)

PRT;

773

Ą

2;

Mismatches

```
"A polymorphic variant in the human electron transfer flavoprotein RT alpha-chain (alpha-T171) displays decreased thermal stability and is RT alpha-chain (alpha-T171) displays decreased thermal stability and is represented in very long-chain acyl-coa dehydrogenase-deficient for the childhood presentation.";

RT overrepresented in very long-chain acyl-coa dehydrogenase-deficient for the mid childhood presentation.";

RT patients with mild childhood presentation.";

RT construction: THE ELECTRON TRANSFER FLAVOPROTEIN SERVES AS A SPECIFIC CCL.
-1- FUNCTION: THE ELECTRONS TO THE MAIN NITOCHONDRIAL RESPIRATORY
CCC TRANSFERS THE ELECTRONS TO THE MAIN NITOCHONDRIAL RESPIRATORY
CCC TRANSFERS THE ELECTRONS TO THE MAIN NITOCHONDRIAL RESPIRATORY
CCC TRANSFERS THE ELECTRONS TO THE MAIN NITOCHONDRIAL RESPIRATORY
CCC TRANSFERS THE ELECTRONS TO THE MAIN NITOCHONDRIAL RESPIRATORY
CCC TRANSFERS THE ELECTRONS TO THE MAIN NITOCHONDRIAL RESPIRATORY
CCC TRANSFERS THE ELECTRONS TO THE MAIN NITOCHONDRIAL RESPIRATORY
CCC TRANSFERS THE ELECTRONS TO THE BRAIN, PLACENTA, LUNG, KIDNEY
CCC TRANSFERS THE ELECTRONS TO THE BRAIN, PLACENTA, LUNG, KIDNEY
CCC TRANSFERS THE ELECTRONS TO THE BRAIN, PLACENTA, LUNG, KIDNEY
CCC TRANSFERS THE ELECTRONS TO THE BRAIN, PLACENTA, LUNG, KIDNEY
CCC TRANSFERS THE ELECTRON THE BRAIN, PLACENTA, LUNG, KIDNEY
CCC TRANSFERS THE ELECTRON THE BRAIN, PLACENTA, LUNG, KIDNEY
CCC TRANSFERS THE ELECTRON THE BRAIN, PLACENTA, LUNG, KIDNEY
CCC TRANSFERS THE ELECTRON THE BRAIN, PLACENTA, LUNG, KIDNEY
CCC TRANSFERS THE ELECTRON THE BRAIN, PLACENTA, LUNG, KIDNEY
CCC TRANSFERS THE ELECTRON THE BRAIN, PLACENTA, LUNG, KIDNEY
CCC TRANSFERS THE ELECTRON THE BRAIN, PLACENTA, LUNG, KIDNEY
CCC TRANSFERS THE ELECTRON THE BRAIN, PLACENTA, LUNG, KIDNEY
CCC TRANSFERS THE ELECTRON THE BRAIN, PLACENTA, LUNG, KIDNEY
CCC TRANSFERS THE ELECTRON THE BRAIN THE BRAIN THE BRAIN THE BRAIN THE BRAIN THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT MET-154.
MEDLINE-99286383; PubMed-10356313;
MEDLINE-99286383; PubMed-10356313;
MINTER V., Nyholm M., Johansen B.N., Minter V., Nyholm M., Johansen B.N., Riberg H., Kolvraa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT MET-154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration the Swiss Institute of Bioinformatics and the EMBL outstation between the Swiss Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its two non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X71129; CAA50441.1; EMBL; X76067; -; NOT_ANNO
                                                                                                                                                                                                                                                                                                                                                                                            proDom; pD003528; ETF_beta;
pROSITE; pS01065; ETF_BETA;
Electron transport; Flavopro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pfam; pro1012; ETF_beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR000049; ETF_beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IIB (GAIIB) (GLUTARICACIDURIA) WHICH RESULTS IN THE EXCRETION NOT IIB (GAIIB) (GLUTARICACIDURIA) WHICH RESULTS IN THE EXCRETION NOT ONLY OF GLUTARIC ACID BUT ALSO OF LACTIC, ETHYLMALONIC, BUTYRIC, AND ISOVALERIC ACIDS. IT IS SEEN IN ISOBUTYRIC, 2-METHYL-BUTYRIC, AND ISOVALERIC ACIDS. IT IS SEEN IN ITSOBUTYRIC, AND ISOVALERIC AND DYSPLASTIC ITS MOST SEVERE FORM IN INFANCY, WITH POLYCOSTIC AND DYSPLASTIC THAT CAN LEAD TO THE MILDER FORM CAIDOSIS AND HYPOGLYCEMIA THAT CAN LEAD TO DEATH. THE MILDER FORM CAN BE CHARACTERIZED BY RECURRENT EPISODES DEASTING LETHARGY OR SLOWLY PROGRESSIVE MYOPATHY.

OF LASTING LETHARGY OR SLOWLY PROGRESSIVE MYOPATHY.

OF LASTING LETHARGY OF THE ETF BETA-SUBUNIT / FIXA FAMILY.
                                                                                                                                                                                                                                                                                                                                                       Disease mutation; Glutaricaciduria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISEASE: DEFECTS IN ETFB ARE THE CAUSE OF GLUTARIC ACIDURIA TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corydon M.J., Andresen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOT_ANNOTATED_CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                flavoprotein; FAD;
                                                                                                                                                                                                                                                                 164
                                                                                                                                                                                                                                                                                                                                              154
                                                                                                                                                                  27843
52.8%;
                                                                                                                                                                                MW.
                                                                                                                                                                           R -> 0 (IN GAIIB)
/FTId=VAR_002369
/7E6EAEF50EB2C80 CRC64;
         Score 38; DB
pred. No. 11;
                                                                                                                                                                                                                                                                                                          /FTId-VAR_008548
                                                                                                                                                                                                                                                                                                                                                                          -
×
                                                                                                                                                                                                                                                                                                                                                                                                                  polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mitochondrion;
                                                                        В
                                                                            بر
4.
                                                                            Length 255
                                                                                                                                                                                                                                                                                                                                                                                                                                    3D-structure.
Indels
             0
                      Gaps
```

6-0CT-2001 (Rel

40,

Last

```
RESULT PTEAM AND ADD DT 0.00 D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                     PTPB_HUMAN STAN
P23467;
01-NOV-1991 (Rel. :
01-NOV-1991 (Rel. :
01-MAR-2002 (Rel. :
                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                          PTPRB
                                                                                                                                                                                                                                                                                    HUMAN
                                                                                                                                              Protein-tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNA-binding; Complete proteome.
DOMAIN 651 720 SI
CONFLICT 754 755
SEQUENCE 773 AA; 85119 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00575; S1; 1.
SMART; SM00316; S1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00316; S1; 1.
PROSITE; PS50126; S1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EcoGene; EG12932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDENTIFICATION BY MASS SPECTROMETRY.
MEDLINE-99420866; PubMed-10493123;
Takacs M.-F., Berndt P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-KI2 / MG1655;

MEDLINE-91426617; PubMed-9278503;

Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mau B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                            12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein yhgF.
YHGF OR B3407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                            GEIQTKPDRVGQA 13
                                                                                                                                                                                                                                                                                                                                                                       GEIQARPEQVDAA 24
                                                                                                   OR PTPB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AE000416;
P05055; 1s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U18997; AAA58204.1; ALT_FRAME. U18997; AAA58205.1; ALT_FRAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complete genome sequence of Escherichia coli K-12."; nce 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 53.8
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shao Y.;
                                                                                                                                                                 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1SRO
                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC76432.1;
                                                                                                                                            phosphatase
                                                                                                                                                                 20, Created)
20, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            yhgF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.8%;
53.8%;
                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ω,
                                                                                                                                          beta precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S1 MOTIF.

OP -> HA (IN REF. 1; AAA58205).
; EA54D9ED952A8229 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
36;
                                                                                                                                                                                                                                                      AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Langen H.,
Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.
                                                                                                                                          (E)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 773;
                                                                                                                                   3.1.3.48) (R-PTP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Takacs B.;
coli by
                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <
                                                                                                                                                                                                                                                                                                                                                                                                                                            0
PRESENTATION OF THE PROPERTY O
                  CARBOHYD
CARBOHYD
                                                              CARBOHYD
CARBOHYD
                                                                                                                                                                     CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                            CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                    DOMAIN
DOMAIN
ACT_SITE
                                                                                                                                                                                                                                                                                                         DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Signal.
SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
```

```
PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00060; FN3; 15.
SMART; SM00194; PTPC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00041; fn3; 16. Pfam; PF00102; Y_phosphatase; 1. PRINTS; PR00700; PRTYPHPHTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003961; FN_III.
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000242; Tyr_prot_phphtase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X54131; CAA38066.1; -. PIR; S12050; S12050.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O - protein tyrosine + Phosphate.

tyrosine + phosphate.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: CONTAINS 1 PROTEIN-TYROSINE PHOSPHATASE DOMAIN.
-!- SIMILARITY: CONTAINS 16 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIM; 176882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a c
between the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tyrosine phosphatases.";
EMBO J. 9:3241-3252(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Krueger N.X., Streuli M., Saito H., "Structural diversity and evolution of human receptor-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=91006018; PubMed=2170109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P18052; 1YFO.
                                                                                                                                                                                                                                                                                                                                                                          817
905
993
1083
1171
1269
1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ransmembrane;
            286
3464
464
640
640
990
990
11082
11082
11352
11947
11904
1172
11904
1172
11904
1172
11904
1172
11904
1172
11904
1172
11904
1172
11904
1172
11904
1172
11904
1172
11904
1172
11904
1172
11904
1172
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11904
11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1997
                                                                                                                                                                                                                                                                                                                                                          FIBRONECTIN TYPE-III 1
FIBRONECTIN TYPE-III 2
FIBRONECTIN TYPE-III 3
FIBRONECTIN TYPE-III 4
FIBRONECTIN TYPE-III 5
FIBRONECTIN TYPE-III 6
FIBRONECTIN TYPE-III 7
FIBRONECTIN TYPE-III 8
FIBRONECTIN TYPE-III 10
FIBRONECTIN TYPE-III 11
FIBRONECTIN TYPE-III 11
FIBRONECTIN TYPE-III 11
FIBRONECTIN TYPE-III 11
FIBRONECTIN TYPE-III 13
FIBRONECTIN TYPE-III 13
FIBRONECTIN TYPE-III 14
FIBRONECTIN TYPE-III 15
   N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                                                                                   N-LINKED
                                                                                                                                                                                                                                                                            N-LINKED
                                                                                                                                                                                                                                                                                                        PROTEIN-TYROSINE BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase; Phosphorylation; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN-TYROSINE PHOSPHATASE
(GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                 PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Usage
   (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                           (POTENTIAL).
                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bу
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   its
```

```
MCH_HAIN1
ID MCH_HAIN1
AC Q9HPD7;
DT 01-MAR-200
NS,NI0-MAR-200
NS,NI0-MAR-200
NS,NI0-MAR-20
NCHITAXID
ACH OR VNG
GN HALOBACTER
OC Archaea; E
OC Archaea; E
OC ARCHAEA;
NCHITAXID
RN [1]
RN SEQUENCE F
RN MEDLINE-20
RN MEDLINE-20
RN ASWARTZell
RN LEithauser
RN ASWARTZell
RN Isenbarger
RN AGMOGCKS D
RN ISENBARGET
CC -i- FUNCTI
CC -i- FUNCTI
CC -i- SIMILA
CC -i- SUBCEL
CC -i- CATALY
CC -i- STMILA

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A My W. Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,

Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,

Swartzell S., Weir D., Hall J., Dahl T.A., Weltl R., Goo Y.A.,

Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,

Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,

Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,

Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,

A Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,

Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;

"Genome sequence of Halbbacterium species NRC-1.;

"Genome sequence of NRC-1.";

"Genome sequence of NRC-1."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O9HPD7:
01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation updat
N5,N10-methenyltetrahydromethanopterin cycl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a copyred through the EMBL between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and formodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
     EMBL; AE005076; AAG19933.1; HSSP; P94954; 1QLM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-20504483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=64091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archaea; Euryarchaeota; Halobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Halobacterium sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MCH OR VNG1686G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Methenyl-H4MPT cyclohydrolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GEIQTKPDRV 10
                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Cytoplasmic (By SIMILARITY: BELONGS TO THE MCH FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSVRTKPDKI 1358
                                                                                 s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 50.0
5; Conservative
                                                                                                                                                                                                                                                                                                                                                        step
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   829
1040
1096
1163
1185
1212
1274
1274
1367
1470
1470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          829
1040
1096
1163
1185
1212
1274
1367
1470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=11016950;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (strain NRC-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       224267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED
N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 38; DB
Pred. No. 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       691E99BA7A1515DD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GLCNAC...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GLCNAC.
(GLCNAC.
(GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        update)
n cyclohydrolase (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GLCNAC. .
                                                                                                                                                              There are no restrictions ong as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Halobacteriaceae,
                                                                                                                                                                                                                                                                                                                            similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.5.4.27)
                                                                                                                                                                                                                      a collaboration -
MBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                for
                                                                                                                                                commercia
                                                                                                                                                                      no
                                                                                                                                                                                             on
                                                                                                                                                                                             its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
```

```
RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QУ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DR
DR
SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mizuseki K., Kishi M., Matsui M., Naka
"Xenopus Zic-related-1 and Sox-2, two
distinct activities in the initiation
Development 125:579-587(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         073689; 057461;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
310-MAY-2001 (Rel. 40, Last annotation update)
21nc finger protein ZIC 1 (Zinc finger protein of the cerebellum (ZIC-related-1 protein) (ZIC-R1) (ODD-paired-like).
ZIC1 OR ZIC-1 OR OPL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metažoa; Chordata; Craniata;
Amphibia; Batrachia; Anura; Mesobatrach
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003209;
Pfam; PF02289; MCH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                 Mech.
                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-98413039; Pub
Nakata K., Nagai T.,
"Xenopus Zic family a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98322239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-98167885; PubMed-9435279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     patterning in Xenopus.";
Development 125:2867-2882(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kuo J.S., Patel M., Gamse J., Me
"Opl: a zinc finger protein that
matterning in Xenonus ":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                     development
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 IQTKPDRVGQAT :||: | | | | |
                                                                                                                                                                                                                       h. Dev. 75:43-51(1998).

h. Dev. 75:43-51(1998).

FUNCTION: MAY PLAY A ROLE IN CEREBELLAR DEVELOPMENT. CAN ACTIVATE FUNCTION: MAY BE USURGOGENIN-RELATED-1, AND INITIATE NEURAL AND THE PRONEURAL GENE NEUROGENIN-RELATED SUFFERENCE AND MAY BE NEURONAL DIFFERENTIATION. MAY MEDIATE NEURAL COMPETENCE AND MEDIAL CREST INVOLVED IN ACTIVATION OF MIDBRAIN, DORSAL NEURAL AND NEURAL CREST FATES; CAN SENSITIZE THE PRESUMPTIVE NEURECTODERM FOR INDUCTION, SUGGESTING THAT IT MAY BE A NEURAL COMPETENCE FACTOR. AN ACTIVATED FORM OF OPL CAN ACTIVATE NEURAL CREST AND DORSAL NEURAL TUBE FORM OF OPL CAN ACTIVATE NEURAL CREST AND DORSAL NEURAL TUBE
CEREBELLUM.

CEREBELLUM. STAGE: FIRST DETECTED AT THE BEGINNING OF DEVELOPMENTAL STAGE: FIRST DETECTED AT THE BEGINNING OF ASTRULATION. IT IS ACTIVATED ZYGOTICALLY BY LATE BLASTULA. ITS GASTRULATION. IT IS EXPRESSION IS MAXIMAL BY MIDGASTRULA, WITH LOWER EXPRESSION PROPERSISTING ANTO TAILBUD STAGES. DURING EARLY GASTRULA STAGES IT I EXPRESSION IN THE PROSPECTIVE EXPRESSION BUILDLY IN THE DORSAL ECTODERM. WHEN NEURAL INDUCTION OCCURS, IT HAS WIDE AND HOMOGENOUS EXPRESSION IN THE PROSPECTIVE REUROECTODERM. LATER, AT LATE GASTRULA STAGES, ITS EXPRESSION IS SHUT OFF IN THE DORSAL MIDLINE EXCEPT IN THE MOST ANTERIOR AREA. AT NEURAL PLATE STAGES, IT IS EXPRESSED IN THE LATERAL PART OF ANTERIOR NEURAL PLATE STAGES, IT IS EXPRESSED IN THE LATERAL PART OF ANTERIOR NEURAL PLATE AND IN THE FLANKING ECTODERM. AT LARVAL
                                                                                                                                                                               SUBCELLULAR LOCATION: Nuclear TISSUE SPECIFICITY: CNS. A HIC
                                                                                                                                                                                                                   ENGRAILED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VQTRVDTVGDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Methanogenesis; 311 AA; 32140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      family and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=9739105;
T., Aruga J., Mikoshiba K.;
ly and its role in neural and neural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=9655809;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51
58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 40
                                                                                                                                                                                  CNS. A HIGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Complete proteome. 
MW; 57A250AAE0E2D3AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mesobatrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ?;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Merzdorf C.,
hat regulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nakanishi S., Sasai Y.;
two factors induced by chordin,
tion of neural induction.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37;
                                                                                                                                                                                    LEVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       À
                                                                                                                                                                                    EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu X., Apekin V., Si neural determination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pipidae;
                                                                                                                                                                                      S
                                                                                                                                                                                                                                                                                                                                                                                                          crest
                                                                                                                                                                                      SEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                      Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                       THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ξ.
                                                                                                       S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
```

```
밁
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 6
                                                                                                                                                                  P26627;
01-AUG-1992 (Rel. 2
01-AUG-1992 (Rel. 2
15-JUL-1999 (Rel. 3
signal.";

J. Virol. 64:6045-6053(1990).

-I- FUNCTION: THE RNA DEPENDENT RNA POLYMERASE OF CORONAVIRUSES IS

-I- FUNCTIONAL PROTEIN: IT CONTAINS THE ACTIVITIES NECESSARY

A MULTIFUNCTIONAL PROTEIN: STRANDED RNA, LEADER RNA,
                                                           Makino S., Yokomori K., Lai M.M.C., "Analysis of efficiently packaged d murine coronavirus: localization of
                                                                                                                                                        01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation updat
RNA-directed RNA polymerase (ORFIA) (EC 2.7
                                                                                                                                                                                                                   CVMJD
                                                                                                                                                                                                                                                                                                                                                                    ZN_FING
ZN_FING
ZN_FING
ZN_FING
ZN_FING
                                                                                       SEQUENCE FROM N.A. MEDLINE-91056574; PubMed-2243386;
                                                                                                                             Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.
                                                                                                                                                Murine coronavirus MHV (strain defective JHM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prim: PF00096; zf-C2H2; 5.

PRINTS; PR00048; ZINCFINGER.

SMART; SM00355; ZnF_C2H2; 4.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.

PROSITE; PS0157; ZINC_FINGER_C2H2_2; 4.

Zinc-finger; Metal-binding; DNA-binding;
                                                                                                                    NCBI_TaxID=11143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                         RRPA_CVMJD
                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                        165
                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                              Neurogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISSP; P08047; 1SP2.
InterPro; IPR000822; Znf-C2H2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ranscription regulation;
                                                                                                                                                                                                                                                                          ٠..
                                                                                                                                                                                                                                                              GEIQTKPDRVGQAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EM European Bioinformatics Institute. There are no restriby non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STAGES,
ITS A-P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE GLI FAMILY OF
                                                                                                                                                                                                                                                       GDMYGRPDQYGQVT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REMOVED INCREASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF022927; AAC14214.1; -. AF028805; AAB99946.1; -. AB009564; BAA33406.1; -.
                                                                                                                                                                                                                                                                                        Similarity 42.9
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAS A CARBOXY TERMINAL INCREASES OPL ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IT IS
AXIS.
                                                                                                                                                                                                                                                                                                                                         AA,
                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DETECTED
                                                                                                                                                                                                                                                                                                                                                          74
80
380
256
292
292
322
352
380
443
                                                                                                                                                                                                                                                                       14
                                                                                                                                                                                                                                                                                                                                         48252 MW;
                                                                                                                                                                                                                                                                                                  51.4%;
42.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Activator; Developmental protein;
                                                                                                                                                                                                                                                                                                                                                                                   POLY-ALA.
POLY-HIS.
ZINC FINGERS.
C2H2-TYPE (ATYPICAL).
C2H2-TYPE (ATYPICAL).
C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAINLY IN THE DORSAL NEURAL TUBE THROUGHOUT
                                                                                                                                                                                                                                                                                        Score 37; DB Pred. No. 30; 4; Mismatches
                                                                                                                                                                                                                                                                                                                                      INCREASES ACTIVITY WHEN MISSING A -> T (IN REF. 2). E6E1CA481CF4Cl06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                             C2H2-TYPE
                                                                                                                                                                                                       PRT;
                                                           ed defective .
n of a possib
                                                                                                                                                     on update) (EC 2.7.7.48) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGULATORY DOMAIN, WHICH
                                                                                                                                                                                                       500
                                                          ective interfering RNAs possible RNA-packaging
                                                                                                                                                                                                                                                                                                DВ
30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   There are no restrictions on as its content is in
                                                                                                                                                                                                       Å
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repeat; Nuclear protein;
                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C2H2-TYPE
                                                                                                                                                                                                                                                                                        4
                                                                                                                                                                                                                                                                                                           Length 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bу
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZINC-FINGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a collaboration -
                                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for
                                                                    of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WHEN
                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             commercia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ņ
                                                                                                                                                                                                                                                                                       0;
          RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                                                                                                                                                               Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                            01-OCT-1989
01-OCT-1989
16-OCT-2001
                                                        SEQUENCE OF 1-23.
                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                            RPL18E
                                                                                                                                                                                                                                                                                                                                                                        P12733;
                                                                                                                                                                                                                                                                                                                                                                                   R18E_HALMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam;
                                                                                                                                                                                                                                                                                             NCBI_TaxID=2238
                                                                                                                                                                                                    N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            {RNA}(N).
```

```
Walsh M.J., McDougall J., Wittmann-Liebold B.;
"Extended N-terminal sequencing of proteins of ribosomes blotted from two-dimensional gels on poly(vinylidene difluoride) membrane.";
                                                                                                                                                          Scholzen T. Arndt E.;
"The alpha-operon equivalent genome region archaebacterium Haloarcula (Halobacterium)
J. Biol. Chem. 267:12123-12130(1992).
                                                                                                                                                                                                                                                                                                                  Hatakeyama T., Kimura M.;
"Complete amino acid sequences of the ribosomal proteins L25, L31 from the archaebacterium Halobacterium marismortui.";
Eur. J. Biochem. 172:703-711(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cotranscribed with genes encoding a tRNA(Leu), the enclase, putative membrane protein in the archaebacterium Haloarcula (Halobacterium) marismortui.";
J. Biol. Chem. 266:24573-24579(1991).
                                                                                               MEDLINE=89062418; PubMed=3196689;
                                                                                                                                                                                                                                                         MEDLINE=92291093;
                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-71 FROM N
                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=88166754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haloarcula marismortui (Halobacterium marismortui).
Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transferase; RNA-directed RNA | NON_TER 500 500 SEQUENCE 500 AA; 55246 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Halobacterial S9 operon. Three ribosomal protein cotranscribed with genes encoding a tRNA(Leu), the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92105119; PubMed=1840597;
Kroemer W.J., Arndt E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50S ribosomal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified and this statement is not removed. entities requires a license agreement (See )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002705; Peptidase_C16.
Pfam; PF01831; Peptidase_C16; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A36388; A36388.
HSSP; P15257; 1LFB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GEIQTKPDRVGQAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBGENOMIC MRNAS AND PROGENY VIRION RNA.
CATALTYIC ACTIVITY: N nucleoside triphosphate =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GQEMTEPDAVGSQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M61144; AAA46451.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 12, Created)
(Rel. 12, Last sequence update)
(Rel. 40, Last annotation update)
al protein L18E (HL29) (L19).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                         PubMed=1376318;
                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=3350019,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B24DB851ED951264 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         дв
35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A
                                                                                                                                                                                    in the extreme marismortui.";
                          of archaebacterial onto glass fiber a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ű
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 500
                       glass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genes are
e enolase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        уd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and
                                                                                                                                                                                                       halophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haloarcula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for
                                                                                                                                                                                                                                                                                                                                                                      L29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
```

```
δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 7; Conser
UNSURE
UNSURE
NON_CONS
NON_CONS
NON_CONS
NON_CONS
                                                                                                                                                                                          MEDLINE-95324511; PubMed-7601088;
Santha R., Savithri H.S., Rao N.A., Vaidyanathan C.S.;
Sartha R., Savithri H.S., Rao N.A., Vaidyanathan C.S.;
"2,3-Dihydroxybanzoic acid decarboxylase from Aspergillus novel decarboxylase.";
                                                                                                                                                                                                                                                                           Eukaryota; Fungi
Eurotiales; Tric
NCBI_TaxID=5061;
                                                                                                                                                                                                                                                                                   Aspergillus niger.

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last anotation update)
0-pyrocatechuate decarboxylase (EC 4.1.1.46)
                                                                                                                                                                                                                                                                                                                                                                                       DHBD_ASPNG STA
P80346;
01-NOV-1995 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ribosomal protein; 3D-structure.
INIT_MET 0 0
SEQUENCE 115 AA; 12291 MW; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest
                                                                                                                        -i- CATALYTIC ACTIVITY: 2,3-dihydroxybenzoate = catechol + CO(2-1- PATHWAY: LAST STEP ITHE METABOLISM OF INDOLE TO CATECHOL.-i- SUBUNIT: HOMOTETRAMER.
-i- MISCELLANEOUS: THE MW OF THE COMPLETE PROTEIN IS ABOUT 38 k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDB; 1FFK; 14-AUG-00.
InterPro; IPR000039; Ribosomal_L18e.
Pfam; PF00256; LL5; 1.
PROSITE; PS01106; RIBOSOMAL_L18E; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M76567; AAA73096.1; -. EMBL; M87833; AAA73213.1; -. PIR; A41715; R5HSH9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20396344; PubMed=10937989; Ban N., Nissen P., Hansen J., Moor
                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                   acid decarboxylase) (DHBD) (Fragments)..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A resolution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochemistry 27:6867-6876(1988)
[5]
                                                                                ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 289:905-920(2000).
-!- SIMILARITY: BELONGS TO THE L18E FAMILY OF RIBOSOMAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete atomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GEIQTKPDRVGQA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTAETKIDQVGEA
                                                                                                                                                                                J. Biochem.
                                                                                                Decarboxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 AA; 12291 MW; 1FE1D7368A7F2AFB CRC64;
 263
247
250
32
66
88
121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                230:104-110(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hansen J., Moore P.B., Steitz T.A.; ic structure of the large ribosomal subunit
 263
247
250
33
67
89
122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36; DB Pred. No. 11; 3; Mismatches
                                                        or
Sk
                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                       ര ര
                                                                                                                                                                                                                                                                                                                                                                                                                      292
                                                                                                                                                                                                                                                                                                                                                                                                                      AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.
                                                                                                                                                                                                                                                                                                                                                 (2,3-dihydroxybenzoic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 115
                                                                                                                           ABOUT 38 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL
                                                                                                                                                                CO(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a collaboration - MBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
```

```
Y825_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 7
                                                                                                                                                               Wray L.V. Jr., Fisher S.H.;
"The Streptomyces coelicolor glnR gene encodes other bacterial response regulators.";
Gene 130:145-150(1993).
-i- SIMILARITY: BELONGS TO THE LACI FAMILY OF J
                                                                                                                                                                                                                                                                                                                                                                Y825_STRCO STANDARD; PRT; 340 AA. 005954; 09KZU3; 01-FEB-1995 (Rel. 31, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Hypothetical transcriptional regulator SCD84.25C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON_CONS
NON_CONS
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON_CONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_CONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_CONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON_CONS
                                                                                  between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                             STRCO
                                             EMBL; L03213; AAA02839.1; PIR; PN0644; PN0644.
                                                                EMBL; AL353816; CAB88491.1; -.
                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                       MEDLINE=93345814; PubMed=7688332;
                                                                                                                                                                                                                                 STRAIN-A3(2)
                                                                                                                                                                                                                                          SEQUENCE OF 1-66 FROM N.A.
                                                                                                                                                                                                                                                             Submitted
                                                                                                                                                                                                                                                                       Rajandream M.A
                                                                                                                                                                                                                                                                                Saunders D.
                                                                                                                                                                                                                                                                                          STRAIN=A3(2);
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                   Actinomycetales; Streptomycineae; NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                        Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                            SCD84.25C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 QIRDKPDRFGAFT 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 EIQTKPDRVGQAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                            (APR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                Harris D., Cerdeno A.M., Parkhill J.,
                                                                                                                                                                        BELONGS TO THE LACI FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33000 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EF78074854BAD925 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                               Streptomycetaceae; Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.
                                                                                                                                                                                                     D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 292;
                                                                                                                                                                                                    protein similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                  Barrell B.G.,
                                                                                                                        restrictions
                                                                                                                                   EMBL
                                                                                                                                     a collaboration -
MBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                              .ch/announce/
                                                                                                                                   outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                        commercial
                                                                                                                                                                                                      ö
                                                                                                                           9
                                                                                                                  តូ
                                                                                                                  way
                                                                                                                           its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
```

InterPro; IPRO0843; HTH_LacI.
InterPro; IPRO00843; HTH_LacI.
Pfam; PF00532; Peripla_BP_like;
SMART; SM00354; HTH_LACI; 1

PS00356;

HTH_LACI_FAMILY; FALSE_NEG.

```
ACCORD REPRESENTED TO THE PROPERTY OF THE PROP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
HYEP_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                          TISSUE-Liver;
Craft J.A., J
                                                                                                          MEDLINE-95137590; PubMed-7835893;
Hassett C., Robinson K.B., Beck N.B., Omiecinski C.J.;
"The human microsomal epoxide hydrolase gene (EPHX1):
nucleotide sequence and structural characterization.";
Genomics 23:433-442(1994).
                                                                                                                                                                                                                                                                                                        ERRATUM.
Hassett (
                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-94282033; PubMed-7516776; Hassett C., Aicher L., Sidhu J.S., Omiecinski "Human microsomal epoxide hydrolase: genetic functional expression in vitro of amino acid Hum. Mol. Genet. 3:421-428(1994).
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     epoxide hydrolase."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jackson M.R., Craft J.A., Burchell B., "Nucleotide and deduced amino acid sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=88015564; PubMed=3502697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JUL-1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Skoda R.C., Demierre A., McBride O.W., Gonzalez "Human microsomal xenobiotic epoxide hydrolase sequence, complementary DNA-directed expression chromosomal localization.";
                                                                       SEQUENCE OF 9-327 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic Acids Res. 15:7188-7188(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wilson N.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1988 (Rel. 07, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Epoxide hydrolase 1 (EC 3.3.2.3) (Microsomal epoxide hydrolase)
(Epoxide hydratase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND SEQUENCE OF 1-19. MEDLINE-88087301; PubMed-2891713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPHX1 OR EPHX OR EPOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYEP_HUMAN P07099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein;
DNA_BIND 6 2
SEQUENCE 340 AA; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ν
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELGYRPDRVAQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EIQTKPDRVGQA 13
                                                                                                                                                                                                                                                                                                      .
C.
         nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 58. 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chem.
                                                                                                                                                                                                                                                                            ., Aicher L., Sidhu J.S., Genet. 3:1214-1214(1994).
    Jackson M.R., Bu:
cleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Omiecinski C.J.;
UL-1988) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263:1549-1554(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AND VARIANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36766 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50
58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transcription regulation; DNA-binding.
5 H-T-H MOTIF (POTENTIAL)
6766 MW; 35F32456E94E1A15 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38;
    Burchell
nce of a c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36; DB Pred. No. 35; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Catarrhini; Hominidae;
  .1 B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIS-113; ARG-139 AND
                                                                                                                                                                                                                                                                                                    Omiecinski C.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Omiecinski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ДВ
35;
    CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                            polymorphism and
variants.";
  for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F.J., Meyer U.A.;
Complementary DNA
in COS-1 cells, a
human liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
; Homo.
                                                                                                                                                            complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ILE-396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cells, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   microsomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
```

```
Q
 В
                                               Matches
                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U06660; 200114.
PIR; 803114; 803114.
PIR; A26856; A26856.
PIR; A29939; A29939.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; J03518; AAA61305.1; -.
EMBL; X07936; CAA30759.1; -.
EMBL; X07936; CAA30759.1; -.
EMBL; Y00424; CAAA6486.1; -.
EMBL; M36374; AAA55580.1; -.
EMBL; L25878; AAA52389.1; -.
EMBL; L25879; AAA52399.1; -.
EMBL; L25879; AAA52399.1; -.
EMBL; U06661; AAB60649.1; -.
EMBL; U06661; AAB60649.1; JOINED.
EMBL; U06658; AAB60649.1; JOINED.
EMBL; U06658; AAB60649.1; JOINED.
EMBL; U06659; AAB60649.1; JOINED.
                                                                                                       CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                         MUTAGEN
MUTAGEN
 305
                                                                                                                                                                                                                                          VARIANT
                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000639; Epox_hydrolase.
InterPro; IPR000379; Est_lip_thioest_actsite.
Pfam; PF00561; abhydrolase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaborate between the Swiss Institute of Bioinformatics and the EMBL outstatise the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a license agreement (See http://www.isb-sib.ch/annot or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT
                                                                                                                                                                                                                                                                                        VARIANT
                                                                                                                                                                                                                                                                                                                       Hydrolase; Endoplasmic reticulum; Detoxification; Transmembrane;
                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00412;
                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000073; Abhydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                 MEROPS; $33.971; -. MIM; 132810; -.
                                                                                                                                                                                                                                                                                                                 iver;
                     5 TKPDRVGQA 13
TKPDTVGSA
                                            l Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                            Aromatic hydrocarbons catabolism; Microsome;
                                            Conservative
                                                                                                                                                                                                                                         396
313
                                                                                                 113
139
112
148
243
348
406
420
52949,
                                                                                                                                                                                                                                                                                                                                    EPOXHYDRLASE
                                                                                                                                                                                                                                         396
                                                                                                                                                                                                                                                               139
                                                          50.0%;
77.8%;
                                                         . 88;
                                                                                                        WW.
                                                                                                                                       /FTIG-VAR_005297.
Y->H: PARTIAL LOSS OF ENZYME ACT!
H->R: SMALL INCREASE IN ENZYME AC
R -> K (IN REF. 3).
R -> N (IN REF. 3).
V -> L (IN REF. 3).
K -> S (IN REF. 3).
                                            0,
                                                        Score 36;
Pred. No.
                                                                                                                                                                                                                           OR A SEQUENCING ERROR).
                                                                                                                                                                                                                                          /FTId=VAR_005296
T -> I (EITHER A
                                                                                                                                                                                                                                                             /FTId=VAR_005295.
H -> R (FREQUENT ALLELE).
                                                                                                                                                                                                                                                                                   Y -> H (FREQUENT ALLELE).
                                                                                                                                                                                                                                                                                                 SIGNAL-ANCHOR (POTENTIAL)
                                            Mismatches
                                                                                                      88E333838C841390 CRC64;
                                                                                                                                                                                                                                         I (EITHER
                                                                                                                 (IN REF. 3).
(IN REF. 3).
                                                   DB 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (See http://www.isb-sib.ch/announce/
                                                                   1;
                                                                                                                                                                                                                                      AN INFREQUENT
                                            2
                                                                   Length 455;
                                            Indels
                                                                                                                                                                                                                                                                                                            Polymorphism
                                                                                                                                                                                                                                      POLYMORPHISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a collaboration -
                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   outstation
                                          0
```

RESULT 12 AF6_HUMAN ID AF6_HUMAN

STANDARD;

PRT;

1816 AA.

```
SMART;
SMART;
SMART;
                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 splicing of the human AF-
DNA Res. 5:115-120(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Croce C.M., Canaani E.; "Cloning of the ALL-1 fusion partner, the AF-6 gene, involved in acute myeloid leukemlas with the t(6;11) chromosome translocation."; cancer Res. 53:5624-5628(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-94061833; PubMed-8242616;
Prasad R., Gu Y., Alder H., Nakamura
Huebner K., Gale R.P., Nowell P.C., F
                                                    Pfam; PF00595; PDZ; 1. Pfam; PF00788; RA; 2. ProDom; PD003376; DIL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Fetal brain; MEDLINE-98344142; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P55196; 075087; 075088; 075089; Q9NU92; 01-0CT-1996 (Rel. 34, Created) 16-0CT-2001 (Rel. 40, Last sequence upd 16-0CT-2001 (Rel. 40, Last annotation u
                                                                                                                                                                                               HSSP;
                                                                                                                                                                                                                                                                                         entities requires a license agreement (or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                     use
                                                                                                                                                                                                                                                                                                                                                   the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (FEB-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 337-1816 FROM N.A. (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF-6 protein
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                 between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genomic structure, DNA polymorphisms, splicing of the human AF-6 gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minami M., Nakamura Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saito S., Matsushima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MLLT4 OR AF6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606
                                                                                                                                      InterPro;
                                                                                                                                                    InterPro;
                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                              MILITED (FEB-2000) to the EMBL/GenBank/DDBJ databases.
FUNCTION: MAY ACT AS AN INTRACELLULAR SIGNALING COMPONEN
CONTROLLED BY RAS SIGNALING PATHWAYS.
SUBUNIT: BINDS DIRECTLY TO 20-1 AND OCCLUDIN.
SUBCELLULAR LOCATION: Cytoplasmic (Probable).
ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1, 2 (SHOWN HERE) AND
PRODUCED BY ALTERNATIVE SPLICING.
DISEASE: INVOLVED IN ACUTE LEUKEMIAS BY A CHROMOSOMAL
THERESULT IS A ROCUE ACTIVATOR PROTEIN.
                                                                                                                                                                                                                                                                                                                   s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation. Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: CONTAINS 1 DILUTE DOMAIN. SIMILARITY: CONTAINS 1 FHA DOMAIN. SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
                                                                                                                                                                                  159559;
                                                                                                                                                                                                                                   AB011399; BAA32484.1; -. AB011399; BAA32483.1; -. AB011399; BAA32485.1; -.
                                                                                                             PF01843; DIL;
                                                                                                                                                                                                             AL049698;
                                                                                                                                                                                                                       U02478; AAC50059
                        SM00240; FHA;
SM00228; PDZ;
              SM003:
                                                                                                                                                                                             2923; 3PDZ
PS50106;
                                                                                                                         IPR002710; DIL.
IPR000253; FHA_domain.
IPR001478; PDZ.
IPR000159; RA.
                                                                                             FHA;
              RA;
                                                                                                                                                                                                             CAB76850.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40, Last sequence update) .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed-9679199;
PDZ; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shirahama S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kuriyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                           (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minaguchi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Canaani
yama K.,
                                                                                                                                                                                                                                                                                                         http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              databases.
NALING COMPONENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O., Saito H.
Miyazaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MLLT4 AND MLL/HRX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kanamori Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ω
```

```
NUM1_
                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                      LT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARSPLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DOMAIN
SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DOMAIN
                                                                                                                                                                "Nuclear migration in Saccharomyces cerevisiae is highly repetitive 313 kDa NUM1 protein."; mol. Gen. Genet. 230:277-287(1991).
                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-ATCC 28383 / FL100;
MEDLINE-92079907; PubMed-1745235;
                                                                                                                                                                                                                                                                                                                                           000402:
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                  Kormanec J., Schaaff-Gerstenschlaeger I.,
Perecko D., Kuentzel H.;
                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Ascomycota; Saccharomycetales; Saccharomyc
                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast):
                                                                                                                                                                                                                                                                                                                     Nuclear migration protein NUM1 OR YDR150W.
                                                                                                                                                                                                                                                                                                                                                                                           NUM1_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIAMOC
                                                                                                                                                                                                                                                                      NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 EIQTKPDR 9
                                           MISCELLANEOUS: ADDITIONAL REGIONS OF LOWER HOMOLOGY TO CONSENSUS (ALMAYS STARTING WITH PROLINE) ARE FOUND IN BEFLANKING DOMAINS OF THE TANDEM REPEATS.
SIMILARITY: CONTAINS 1 PH DOMAIN.
CAUTION: IT IS UNCERTAIN WHETHER MET-1 IS THE INITIATOR.
                                                                                                                FUNCTION: CONTROLS NUCLEAR MIGRATION. NUM1 SPECIFICALLY CONTRE INTERACTION OF THE BUD NECK CYTOSKELETON WITH THE PRE-
DIVISIONAL G2 NUCLEUS PERHAPS BY RECOGNIZING G2-SPECIFIC CYTOPLASMIC MICROTUBULI OR OTHER COMPONENTS OF THE NUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELOSKPDR 1532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 75.6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1612
1666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translocation;
                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1408
A; 205604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1816
373
391
391
744
1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              491
910
1077
174
1356
1376
1571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1816
1743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1611
                                                                                                                                                                                                                                                                                    Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50
75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISOFORM 3).

MISSING (IN ISOFORM 3).

G -> V (IN REF. 1).

P -> PGRRNHFAYYNYHTYE (II

D -> DSSHFD (IN REF. 3).

D -> DV (IN REF. 1).

R -> P (IN REF. 1).

R -> P (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                    NUM1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proto-oncogene; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LCRPPLPRDYEPPSPSPAPGAPPPPPQRNASYLKTQVLSPD
SLFTAKFVAYNEEEEEEEDCSLAGQDKYSSTRKSHGDL ->
PNSYPGSTGAAVGAHDACRDAKEKRSKSQDADSPGSSGAPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PILASACFPWG (IN ISOFORM 1).
MISSING (IN ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NLTFKERQRLFSQGQDVSNKVKASRKLTELENELNTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MLL FUSION POINT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DILUTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LQDEERRRQQQLEEMRKREAEDRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LEUKEMIA PATIENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASP/GLU-RICH (ACIDIC)
                                                                                                                                                                                                                                                                                    Saccharomycotina; Saccharomycetes; cetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -> V (IN REF. 1).
-> PGRRNHFAYYNYHTYE (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EB1FE7F04879CE8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No.
                                                                                                                                                                                                                                                                                                                                                                                             2748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                             A
                                                                                                                                                                                                                2immermann F.K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (IN AN ACUTE MYELOID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1816;
                                                                                  HOMOLOGY TO THE
                                                                                                                                            SPECIFICALLY CONTROLS ON WITH THE PRE-
                                                                                                                                                                                          controlled by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ţ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VKGGVLWLCPSVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
 L outstation -
                                                                                                REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                           the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
```

Swiss Institute Bioinformatics

Institute.

are

restrictions

REPEAT REPEAT REPEAT

1384 656 727

12.5

X TANDEM REPEATS.

DOMAIN Repeat

PROSITE;

PS50003;

PH_DOMAIN;

InterPro; IPR001849; PH. Pfam; PF00169; PH; 1. SMART; SM00233; PH; 1.

EMBL; X61236; CAA43554.1; .

\$19052; \$19052. \$0002557; NUM1.

entities requires a license agreement (Some or send an email to license@isb-sib.ch).

institutions as long tatement is not removed. license agreement (See

as its content

ST

Usage

modified and this st

```
(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in
                                                                                                                                                                                                                                                                                                                                                                                0;
                             J. Bacteriol 171:4448-4456(1989)
-I- FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM HYDH/HYDG
IN THE REGULATION OF THE LABILE HYDROGENASE ACTIVITY.
PHOSPHORYLATES HYDG IN RESPONSE TO ENVIRONMENTAL SIGNALS.
THAT
                                                      "Initial cloning and sequencing of hydrig, an operon homologous to coli K-12.",
                                                                                                                                                                                                                                                                                                                            HYDH_ECOLI
                                                                                                                                                                                                                                                                                                                                    RESULT 15
                                                                                                                                                                                                                                                                                                                                                                DЪ
                                                                                                                                                                                                                                                                                                                                                                               Ş
                                                                                                MEDIINE-89327164; PubMed-2666400;
                                                                                                                   SEQUENCE OF 328-465 FROM N.A.
                                                                                                                      "Analysis of the Escherichia coli genome. IV. DNA sequence region from 89.2 to 92.8 minutes.";
Nucleic Acids Res. 21:5408-5417(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 48.6
Matches: 6; Conservative
                                                                                                                                                                     Blattner F.R., Burland V.D.,
                                                                                                                                                                                     MEDLINE 94089392; Pu
                                                                                                                                                                                                                                                        01-JAN-1990 (Rel. 13, Created)
01-OCT-1993 (Rel. 27, Last seq
01-MAR-2002 (Rel. 41, Last ann
Sensor protein hydH (EC 2.7.3
                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                               Escherichia coli
                                                                                                                                                                                                                                                                                                        HYDH_ECOLI
P14377;
                                                                                                                                                                                                      EQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                   175 GVKEDKPEEIGQAS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA_BIND
ZN_FING
ZN_FING
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00398; STRDHORMONER.
PRINTS; PR00047; STRDIDFINGER.
SMART; SM00430; HOLI; 1.
SMART; SM00399; ZNF_C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zinc-finger; Multigene family; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Receptor; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                   1 GEIQTKPDRVGQAT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00031; NUCLEAR_RECEPTOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterProj IPR001628; zf-C4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-slb.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000536; Hormone_rec_lig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                     395
                                                                                                                                                                                                                                                                                                                                                                                                                                             32
32
70
149
                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                               PubMed=8265357;
rland V.D., Plunkett G.
                                                                                                                                                                                                                                                                                                                                                                                                                                   ΑĄ,
                                                                                                                                                                                                                                                            27, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                           48.68;
42.98;
                                                                                                                                                                                                                                                                                                                                                                                                                            45113 MW;
                                                                                                                                                                                                                                                        2.7.3.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strdhormone_receptor.
                                                                                                                                                                                                                                                                                                                                                                                     Score 35; DB Pred. No. 63;
                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                               LIGAND-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEAR RECEPTOR-TYPE.
C4-TYPE.
C4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                 F4319CDF96FE2451 CRC64;
                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                465 AA.
                                                                                                                                                                                                                                                               update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA-binding; Nuclear
                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                           4.
                                                                                                                                                                                                                                                                                                                                                                                       Length 395;
                                                                                                                                                                                                                                                                                                                                                                      Indels
momb -- ..
                                                                                                                                      of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein;
                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page
                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Φ
```

THB_PAROL

THB_PAROL 091279;

STANDARD;

PRT;

395 AA.

.5-JUL-1999 (Rel. 38, Created)

밁 Ş

2441 LTTKEDKKGQAT 2452

3 IQTKPDRVGQAT 14 Local Similarity es 7; Conserv

Conservative

50.08; 58.38;

Score 36; DI Pred. No. 3.

Mismatches

лв ₊, 3.2e+02; 3; DB 1;

Length 2748;

Indels

0,

Gaps

Matches Ouery Match

REPEAT REPEAT REPEAT

REPEAT REPEAT REPEAT REPEAT

REPEAT REPEAT REPEAT

SEQUENCE DOMAIN

AΑ;

313202 MW; B2FBD67C9F6211AE CRC64;

(INCOMPLETE).

2683

This SWISS-PROT entry is copyright. between the Swiss Institute of Bio -!- SUBCELLUILA LOCATION: Nuclear.
-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; BETA-1 (SHOWN HERE) AND BETA-2;
-!- DOMAIN: COMPOSED BY ALTERNATIVE SPLICING.
-!- DOMAIN COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
-- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY. "CDNA cloning of thyroid hormone receptor beta for the Japanese Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Neoteleostei; Percomorpha; Pleuronectiformes; Paralichthys Olivaceus (Flounder). Thyroid hormone receptor beta (THR-beta). 15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update) Comp. Endocrinol. 99:197-203(1995).
FUNCTION: HIGH AFFINITY RECEPTOR FOR TRIIODOTHYRONINE. PubMed=8536930; Bioinformatics is produced through a collaboration ormatics and the EMBL outstation -Neoteleostei;

MEDLINE-96149097; Yamano K., Inul Y.

SEQUENCE FROM N.A.

Gen. flounder.";

```
CC (Probable).
CC (Probable).
CC (1- SINILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
CC (1- SINILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
CC (1- SINILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
CC (1- SINILARITY: CONTAINS INSTITUTE of BROADCREE HISTIDINE CONTAINS (1- CONTAINS CONT
```

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
AAG90736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                              Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                           WPI; 2001-376931/40.
N-PSDB; AAH65955.
                                                                                                                                                                                                                                                                                                                                                                                                             Coryneform bacterium; amino acid synthesis; vitamin; organic acid synthesis.
            Claim
                                                                                                                                                                                                                                                                                                                                                    EP1108790-A2
                                                                                                                                                                                                                                                                                                                                                                                 Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                        C glutamicum protein fragment SEQ ID NO: 4490.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAG90736 standard; Protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 13; SEQ
                                                                                                                                                      Nakagawa S,
Tateishi N,
                                                                                                                                                                                                                               03-AUG-2000;
                                                                                                                                                                                                                                             07-APR-2000;
                                                                                                                                                                                                                                                                                        18-DEC-2000; 2000EP-0127688
                                                                                                                                                                                                                                                                                                                       20-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG90736;
                                                                                                                                                                                                 (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                                                                                                                           16-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 sdgvytmes 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDGFYTMEN 10
          17;
          SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 AA;
                                                                                                                                                                                                                           ; 99JP-0377484.
; 2000JP-0159162.
; 2000JP-0280988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                      Mizoguchi H,
Senoh A, Ik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
            Ħ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ID 4314; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                 glutamicum
            <u>N</u>O:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47.5%;
77.8%;
          4490;
                                                                                                                                                      Ikeda
       246pp + Sequence Listing; English
                                                                                                                                                    Ando S, Hayashi M,
da M, Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ۲
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 38; DB Pred. No. 47; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                    Ochiai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           saccharide;
                                                                                                                                                                    Yokoi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
```

Search completed: June 10, Job time: 168 sec

2002, 15:21:08

```
Дb
                               Q
                                                                    Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                           from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine: The present sequence is a protein described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                    sequences from the Coryneform bacterium Corynebacterium glitamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived
                                                                                                                                                                     Sequence
                                                                                                                                                                                                      European
                                                                                                                                                                                                                        Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides a number of nucleotide and
94 lssgfftven 103
                                   1 MSDGFYTMEN 10
                                                                                                                                                                                                      Patent Office.
                                                                                                                                                                     135 AA;
                                                                                          47.5%;
                                                                        ω
••
                                                                                        Score 38;
Pred. No.
                                                                        Mismatches
                                                                                    05;
                                                                                                            22;
                                                                                                          Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                protein
                                                                        0;
                                                                    Gaps
                                                                        0
```

```
Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM protein -
                                                                                                                                                                                                                                                                                       Result
                                                                                                                                                                                                                                                                                                                                                                                                 Database
                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        on
On
score
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
Bd
                                                                                                                                                                                                                                                                              Score
                                                                                                                                                                                                                                                                                                                           is
                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq
                                                                                                                                                                                                                                                                                                                          s greater t
is derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein search, using sw
                                                                                                                                                                                                                                                                                                                                                                                                                                                      length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                        is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution.
                                                                                                                                                                                                                                          100.0
53.8
52.5
                                                                                                                                                                                                                                                                                      Query
                                                                                                                                                                                                                                                                              Match
                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum Match 0%
Maximum Match 100%
Listing first 45 s
June 10, 2002, 15:22:24; Search time 35.61 Seconds (without alignments) 40.476 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                 PIR_71:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  283138 seqs, 96089334 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-647-522-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MSDGFYTMENSDRRK 15
                                                                                                                                                                                                                                                                                                                                                             pir1:*
pir2:*
pir3:*
pir4:*
                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.0 ,
                                                                               376
437
704
704
704
160
160
164
187
339
357
387
                                                                                                                                                                                                                       387
                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gapext 0
                                                                                                                                                                         AD2585
C75632
H82012
                                           E90748
A85599
                                                                                                                                              JQ1866
G95213
                                                                                                                                                                D81240
                                                             DEECPC
                                                                                                                                                                                                     C97367
                                                                                                                                                                                                                                                                             ij
                                                                       E84579
                                                                                        T4862
                                                                                                          S63142
                                                                                                                                                                                                                                                                                                                                                                                                                    summaries
                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  283138
                       pyruvate dehydroge
pyruvate oxidase [
pyruvate oxidase p
pyruvate dehydroge
probable thiamine
                                                                    hypothetical prote
recr protein [impo
hypothetical prote
hypothetical ww do
hypothetical prote
                                                                                                                           hypothetical prote glycerol-3-phospha
                                                                                                                                                                       probable hemolysin capsule polysaccha
                                                                                                                                                                                           DNA replication an
                                                                                                                                                                                                             vesicular transpor
                                                                                                                                                                                                                               SSU ribosomal
                                                                                                                                                                                                                                                                            Description
              hypothetical prote
                                                                                                                  probable fructose-
                                                                                                                                              hypothetical
                                                                                                                                                       hypothetical
                                                                                                                                                                 capsule
                                                                                                                                                                                                                                         carboxylesterase
                                                                                                                                                                                                                                                  chitinase
                                                                                                                                                                                                    recF protein
                                                                                                                                                                                                                       hypothetical
                                                                                                                                                       polysaccha
ical 87.1K
                                                                                                                                                                                                                                                  jellyfish
e (EC 3.2
                                                                                                                                              prote
                                                                                                                                                                                                    odmi]
                                                                                                                                                                                                                                prot
```

45	44	. 43	42	41	40	39	38	37	36	35	34	33	32	31	30
37	37	37	37	. 37	37	37	37	37	37	37	37	38	38	38	38
46.2	46.2	46.2	46.2	46.2	46.2	46.2	46.2	46.2	46.2	46.2	46.2	47.5	47.5	47.5	47.5
561	550	544	520	520	520	421	265	228	221	210	49	687	687	520	464
1	ب	N	N	N	N	N	N	N	N	۳	N	N	N	2	N
S34191	VGIHD6	S41626	S14598	S14600	S14599	AI2090	D82871	T51147	H84781	Z7BPT9	D97048	E81027	G81970	T06625	T39699
												•			
sulfite reductase	E2 glycoprotein pr	spike protein chai	E2 glycoproteir	E2 glycoproteir	E2 glycoprotein	two-component resp	conserved hypothet	hypothetical	hypothetical	gene 55.10 protein	hypothetical	glycyl-tRNA synthe	probable glycine	hypothetical	glutathione reduct

ALIGNMENTS

```
Chitinase (EC 3.2.1.14) precursor - Orgyia pseudotsugata nuclear polyhedrosis virus (Species: Orgyia pseudotsugata nuclear polyhedrosis virus, OpMNPV (C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000 (Accession: T10393 **
R;Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F. Virology 229, 381-399, 1997
A;Title: The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedro A;Reference number: Z17011; MUID:97271300
A;Accession: T10393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            toxin - jellyfish (Carybdea rastoni)
C;Species: Carybdea rastoni
C;Species: Carybdea rastoni
C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 17-Nov-2000
C;Accession: JC7371; PC7094
R;Nagai, H; Takuwa, K.; Nakao, M.; Ito, E.; Miyake, M.; Noda, M.; Nakajima, T.
Blochem. Blophys. Res. Commun. 275, 582-588, 2000
A;Title: Novel proteinaceous toxins from the box jellyfish (sea wasp) Carybdea raston
A;Reference number: JC7371
A;Accession: JC7371
                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
T10393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein
A; Residues: 39-55;56-70;196-210;250-267;268-279;309-325;363-377;378-382 <NA2>C; Comment: This protein, a member of bloactive protein, has hemolytic activity C; Keywords: hemolysis; inflammation; toxin
A;Cross-references: EMBL:U75930; NID:g2934903; PIDN:AAC59123.1; C;Superfamily: Serratia marcescens chitinase C;Keywords: glycosidase; hydrolase; polysaccharide degradation
                                                                                          A; Molecule type: DNA
A; Residues: 1-550 < AHR>
                                                                                                                                      A; Status: preliminary; translated from GB/EMBL/DDB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       엉
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-450 <NAG>
A; Cross-references: DDB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: PC7094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    363 MSDGFYTMENSDRRK 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSDGFYTMENSDRRK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DDBJ:AB015878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 80;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 450;
                                                             PID:g1911370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
```

Best Local S
Matches 7

7; Conserv

Conservative

53.8%; 46.7%;

Score 43; DB Pred. No. 14; 5; Mismatches

Length 550

Indels

0;

Gaps

```
R/She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Al
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng,
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Field, L.M.; Williamson, M.S.; Moores, G.D.; Devonshire, A.D. Blochem. J. 294, 569-574, 1993

A;Title: Cloning and analysis of the esterase genes conferring A;Reference number: S36786; MUID:93384534

A;Accession: S36786
 hypothetical protein yycP - Bacillus subtilis (;Species: Bacillus subtilis C;Species: Bacillus subtilis C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000 C;Accession: D70090 R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedc C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X74554; NID:g397510; C;Superfamily: cholinesterase; cholinesterase C;Keywords: carboxylic ester hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSU ribosomal protein S6E (rps6E) [imported] - Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
D90185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-552 <FIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       carboxylesterase (EC 3.1.1.1) E4 - gree C; Species: Myzus persicae (green peach C; Date: 09-Jun-1994 #sequence_revision
                                                                                                                         RESULT
D70090
                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-214 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: A99139
A; Accession: D90185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;52-552/Domain: cholinesterase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: S36786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                      δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: D90185
                                                                                                                                                                                                    맑
                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                               Genetics:
                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 474 DGFYVYDNEEDRK
                                                                                                                                                                                                    182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            266 LSDPFYFMHDADKRR 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ω
                                                                                                                                                                                                                                                                                                                                                                           rps6E
                                                                                                                                                                                                                                          4 GFYTMENSDRRK 15
                                                                                                                                                                                                    GFYPNENGERRR 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DGFYTMENSDRRK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MSDGFYTMENSDRRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 7; Conserv
                                                                                                                                                                                                                                                                                Similarity 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               GB:AE006641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.5%;
                                                                                                                                                                                                                                                                                                  51.2%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      homology <CHE>
                                                                                                                                                                                                                                                                                                                                                                                                               NID:g13813563; PIDN:AAK40739.1; GSPDB:GN00155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
                                                                                                                                                                                                                                                                                                Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              green
                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 en peach aphid
aphid)
01-Dec-1995 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                            DB
12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIDN:CAA52648.1; homology
                                                                                                                                                                                                                                                                                                                  2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 552;
                                                                                                                                                                                                                                                                                                                  Length 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y.; Allard, G.; Away
Peng, X.; Thi-Ngoc,
m.; Alloni, G.; Azevedo,
B.; Capuano, V.; Carter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PID:g397511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             insecticide resistance
                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Awayez, M.J.;
goc, H.P.; Red
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
     Carter,
                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
     N. M. .
                         Berter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chan:
                                                               밁
       RESULT
```

```
A,Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galicch, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau y, M.; Ogawa, K.; Ogivara, A.; Oudega, B.; Park; S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Cakuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya T.; Winters, P.; Wipat, A.; Yanamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida A; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A; Reference number: A69580; MUID:98044033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Biol. Chem. 269, 8408-8415, 1794
A;Title: Identification of membrane-associated
A;Reference number: A53435, MUID:94179225
A;Accession: B5345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
B53435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QΥ
δÃ
                                                                                                                                                                          C;Keywords: tandem repeat F;74-557/Region: 8-residue repeats
                                                                                                                                                                                                                                                                                                                                                       R;Lee, M.; Russell, D.; d'Alesandro, P.; v
submitted to the EMBL Data Library, Decemb
A;Description: Identification of membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-189,558-721,'P',723-738,'D',740-829,'L',831-1100,'Q',1102-1636,'L'
418,'H',2420-2499,'L'_____
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 26-May 1995 #sequence_revision 07-Jul-1995 #text_change 07-May-1999
C;Accession: B53435; S34395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N;Alternate names: membrane-associated C;Species: Trypanosoma brucei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vesicular transport-associated repeat protein Tb-292 - Trypanosoma brucei N; Alternate names: membrane-associated protein Tb-292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-387 <KUN>
A; Cross-references: GB:
                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-2550 <LEE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                               A;Cross-references: EMBL:X73956; NID:g393395; PID:g393396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Lee, M.G.S.; Russell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 390,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A.; Ehrlich,
                                                                                                                                                                                                                                                                                                             A; Accession:
                                                                                                                                                                                                                                                                                                                             A; Reference number: S34394
                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: EMBL: X73956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: nucleic acid sequence not shown
                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 TDGFYTLYNS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                            Local
1 MSDGFYTMENSDRRK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 SDGFYTMENS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        уусР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249-256,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; 249-256, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 7; Conserv
                                                 Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                             S34395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus subtilis hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Russell, D.G.; D'Alesandro, P.A.; Van der Ploeg, L.H.T 269, 8408-8415, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GB:Z99124; GB:AL009126; NID:g2636442; PIDN:CAB16064.1; PID:g26365ce: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.2%;
                                                                            51.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41;
Pred. No.
                                                 ω,
                                                 Score 41; DB 2;
Pred. No. 1.6e+02;
3; Mismatches 5
                                                                                                                                                                             (A-R-L-R-A-E-E-E)
                                                                                                                                                                                                                                                                                                                                                                                  , P.; van der Ploeg,
December 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                          associated proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein yych
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proteins
                                                 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 387
                                                                                                 Length 2550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in Trypanosoma brucei encodin
                                                                                                                                                                                                                                                                                                                                                             ί'n
                                                                                                                                                                                                                                                                                                                                                          Trypanosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ferrari,
                                                                                                                                                                                                                                                                                                                                                               brucei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                 0
```

2237 MADGCYAVSREDRQK 2251

```
S.; Smit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen
A; Reference number: A97359; PMID:11743194
A; Accession: C97367
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-376 <KUR>
                                                       R; White,
                                                                      probable hemolysin - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: C75632
                                                                                                                                                                                                                                                                                                                                                                           A; Gene: recF
A; Map position
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number:
A; Accession: AD2585
A; Status: preliminar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ster, E.W.
A;Titte: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58
A;Reference number: AB2577; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Woc
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.;
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA replication and repair protein recf [imported] - Agrobacterium tumefacie C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002 C;Accession: AD2585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: AGR_C_109
A; Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE007869; C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Goodner, B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision
C:Accession: C97367
                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE008688; PIDN:AAL41098.1; PID:g17738389; GSPDB:GN00186 A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-376 <KUR>
                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Authors: Yoo, H.; Tao,
                                                                                                                                                                                                                                                                                                                                                                                                                    ;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                    Smith,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein (imported) - Agrobacterium tumefaciens (strain C58,
te, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, Shen, M.; Vamatheyan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, nith, H.O.; Venter, J.C.; Fraser, C.M. ce 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132
                                                                                                                                                                                                                    132
                                                                                                                                                                                                                                                                                                                                                                             position: circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity hes 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      w
                                                                                                                                                                                                                                                      ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preliminary
                                                                                                                                                                                                                    DGLFTGSSSDRRR 144
                                                                                                                                                                                                                                                      DGFYTMENSDRRK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DGFYTMENSDRRK
                                                                                                                                                                                                                                                                                       Similarity 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hinkle, G.; Gattung, S.;
Mollam, C.; Allinger, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15
                                                                                                                                                                                                                                                                                                                                                                               chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.0%;
                                                                                                                                                                                                                                                                                                          50
                                                                                                                                                                                                                                                                                                      . 0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        w
••
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIDN: AAK85892.1;
                                                                                                                                                                                                                                                                                       ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                        Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-Sep-2001 #text_change 11-Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Miller, N.;
Doughty, D.;
                                                                                                                                                                                                                                                                                                        No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
32;
                                                                                                                                                                                                                                                                                                    рв
32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and
                                                                                                                                                                                                                                                                                                                         2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PID:g15154937;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biotechnology
                                                                                                                                                                                                                                                                                       ω
••
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Blanchard, I; Scott, C.;
                                                                                                                                                                                                                                                                                                                       Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wood, G.E.; Chen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M.; Qurollo,
; Lappas, C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Levy, R.; Li,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cereon)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSPDB:GN00169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Agent Agrobacterium
                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B.; Goldn
Markelz,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :
:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goldman,
ckelz, B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McClel
                                       O M
                                       ٠. ن
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ę
```

```
A; Map position: megaplasmid
A; Genome: plasmid
A; Note: plasmid MP1
C; Superfamily: hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Genome sequen
A;Reference number: A7
A;Accession: C75632
A;Status: preliminary
                                                                                                                                                                                                                               A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis A;Reference number: A81775; MUID:20222556 A;Accession: H82012
δÃ
                                                                                                                                                 A;Cross-references: GB:AL162752; GB:AL157959; NID:g7378778; PIDN:CAB83501.1; PID:g737
A;Experimental source: serogroup A, strain Z2491
                                                                                                                                                                                                                                                                               ; Holroyd, S.; Jagels, K.; Nature 404, 502-506, 2000
                                                                                                                                                                                                                                                                                                             C; Accession: H82012
R; Parkhill, J.; Acht
                                                                                                                                                                                                                                                                                                                                              C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                          capsule polysaccharide modification protein NMA0186 [imported] - Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: GB: AE001826; A; Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-437 <WHI>
                                                                                                                   A; Gene:
                                                                                                                                                A; Experimental source: serogroup
                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-704 < PAR>
                                                                                                                                                                                                                A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                H8201
                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: DRB0128
                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 347 SDGFWIQENGD
                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                 10
 2 SDGFYTMENSDRRK 15
                                                                                                                 lipA; NMA0186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 SDGFYTMENSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome sequence of the radioresistant bacterium Deinococcus radiodurans nce number: A75250; MUID:20036896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 7; Conserv
                                 Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                 Achtman, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50.0%;
                                                 50.0%;

    James,
Leather,

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NID:g6460827; PIDN:AAF12559.1; PID:g6460855; TIGR:DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>,,</u>
                                                 Score 40; DB
Pred. No. 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40;
                                                                                                                                                                                                                                                                                              K.D.; Bentl
S.; Moule,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HI0107
                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No.
                                                                                                                                                                                                                                                                                            Bentley, soule, S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
                                                                DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2;
                                                                  2;
                                                                                                                                                                                                                                                                                              Mungall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ω
--
                                                                                                                                                                                                                                                                                                                 S.D.;
                                                                  Length 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                   Indels
                                                                                                                                                                                                                                                                                            Churcher,
                                                                                                                                                                                                                                                                                            er, C.;
Quail,
                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                   Gaps
                                                                                                                                                                                                                                                                                                M.A.;
                                                                                                                                                                                                                                                                                                                                                                                 meningitid
                                                                                                                                                                                                                                                                                              S.R.; Mo
Rajandre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R1
```

```
A; Molecule type: DNA
A; Residues: 1-704 <TET>
A; Cross-references: GB:
                                                                                                                           A; Authors: Grandi, G.; Sun, L.; Smith, H.O.; F: A; Title: Complete genome sequence of Neisseria A; Reference number: A81000; MUID:20175755
                                                                                                                                                                                                                                                                                                   C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision
C;Accession: D81240
                                                                                                                                                                                                       ri, H.; Qin, H.; Vamathe Science 287, 1809-1815,
                                                                                                                                                                                                                            R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eiser Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
                                                                                                                                                                                                                                                                                                                                                                             capsule polysaccharide modification protein LipA NMB0082 [imported] - Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                              A;Status: preliminary
                                                                                                   A; Accession: D81240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDGLOSINNNNRRK 18
                                                                                                                                                                                                          2000
                                                                                                                                                                                                                                                                                                                                31-Mar-2000 #text_change
                                                                                                                                                                             Fraser, C.M.;
                                                                                                                                                   meningitidis
                                                                                                                                                     Moxon, E.R.
serogroup
                                                                                                                                                                                                                                                                                                                                19-Jan-2001
                                                                                                                                                        В
                                                                                                                                                     Rappuoli, R.;
strain MC58.
                                                                                                                                                                                                                                                 Eisen,
```

menin

GB:AE002368; GB:AE002098;

NID: g7225303;

PIDN: AAF40546.1;

PID: 9722

```
RESULT 12
JO1866
hypothetical 87.1K protein - bovine adenovirus 3
C:Species: Mastadenovirus bos3 (bovine adenovirus 3)
C:Date: 14.Jul-1994 #sequence_revision 14.Jul-1994 #text_change 07.May-1999
C;Accession: JQ1866
R;Mittal, S:K.; prevec, L.; Babiuk, L.A.; Graham, F.L.
J. Gen. Virol. 73, 3295-3300, 1992
A;Title: Sequence analysis of bovine adenovirus type 3 early region 3 and fibre protein A;Reference number: PQ0499; MUID:93107871
A;Accession: JQ1866
A;Molecule type: DNA
A;Residues: 1833 (MIT)
A;Cross-references: DDBJ:D12928
A;Experimental source: strain WBR-1
A;Note: the authors described carbohydrate binding site for residue 574
 밁
                               QV
                                                                                                                                                     A;Molecule type: DNA A;Residues: 1-160 <KUR>
A;Residues: 1-160 <KUR>
A;Cross-references: GB:AE005672; PIDN:AAK75904.1; PID:g14973332; GSPDB:GN00164; A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP1831
                                                                                                                                                                                                                                                                                             A; Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, A; Title: Complete Genome Sequence of a virulent isolate of Streptococcus A; Reference number: A95000; MUID:21357209; PMID:11463916
                                                                                                                                                                                                                                                                                                                                                   on, J.D.; Umayam, L.A.; White, nson, T.; Hickey, E.K.; Holt, 1 Science 293, 498-506, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein SP1831 [imported] - Streptococcus pneumoniae (strain T c;Species: Streptococcus pneumoniae C;Species: Streptococcus pneumoniae C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001 C;Accession: G95213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: C; Genetics: A; Gene: NMB0082
                                                                                                                                                                                                                                                                              A; Reference number: A95000; A; Accession: G95213
                                                                                                                                                                                                                                                                                                                                                                                      R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                            A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 7
                                                                    Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 MSDGLYTKDN 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MSDGFYTMEN 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 SDGFYTMENSDRRK 15
MSDGFYEFYQNNQNK 128
                               MSDGFYTMENSDRRK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDGLQSINNNNRRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . Similarity
7; Conserv
                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 serogroup
                                                                                                                                                                                                                                                                                                                                                                       Holt, I.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18
                                                                                    48.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.0%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B, strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
Pred.
                                                                                    Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 40;
Pred. No.
                                                                  core 39; DB red. No. 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                   2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2;
                                                                  5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2
                                                                                                   Length 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pneumoniae (strain TIGR4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                        Read,
M.R.;
                                                                                                                                                                                                                                                                                                                                                                                    T.D.; Pe
Radune,
                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                Peterson, S.; Heie, D:; Holtzapple,
                                                                                                                                                                                                                                                                                                                B.A.; Morrison pneumoniae.
                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                          TIGR: SP
                                                                                                                                                                                                                                                                                                                                                                                                        Hei
                                                                                                 Search completed:
Job time: 206 sec
                                                                                                                                                                                        В
                                                                                                                                                                                                                       δδ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
```

```
Ring, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G. Jung, K.H.; Alam, M.; Freitas, T. Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A; Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, A; Title: Genome sequence of Halobacterium species NRC-1.
A; Reference number: A84160; MUID:20504483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6. A;Reference number: A97872; MUID:21429245; PMID:11544234 A;Accession: H98077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein spr1650 [imported] - Streptococcus pneumoniae (strain C;Species: Streptococcus pneumoniae C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001 C;Accession: H98077
                                                                                                                                                                                                        A; Gene:
                                                                                                                                                                                                                                             A;Residues: 1-187 <STO>
A;Cross-references: GB:AE004437; NID:g10580619; PIDN:AAG19473.1;
                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-187 <S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: E84263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glycerol-3-phosphate dehydrogenase chain A [imported] - Halobacterium sp. C; Species: Halobacterium sp. NRC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-164 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren,
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
                                                                                                                                                                                                                               C; Genetics:
                                                                                                                                                                                                                                                                                                                                           A; Reference number: A; Accession: E84263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary
                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references:
                                                                                    Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 7; Conserv
103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 MSDGFYEFYQNNQNK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14
                                          1 MSDGFYTMENSDR 13
                                                                                                                                                                                                     gpdA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSDGFYTMENSDRRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  spr1650
ISRGFYVLDHADR 115
                                                                                       similarity
6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GB:AE007317; PIDN:AAL00453.1; PID:g15459321; GSPDB:GN00174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48.8%;
46.7%;
                                                                                                                4 6
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15
                                                                                                              28
                                                                                                              Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 39; DB
Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                         Mismatches
                                                                                                                                   DB
                                                                                                                                   2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>ن</u>
                                                                                         2.
                                                                                                                                 Length 187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 164
                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D.W.; Maddocks, D.G.;
                                                                                                                                                                                                                                                    GSPDB: GN00138
                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jaskunas,
                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                           T.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lasky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B.S.
```

June 10, 2002, 15:22:26

```
Minimum
Maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           o
    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
                                                                                                                                  36
36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq
                                                                                                                                                                            377377
377377
377377
377377
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37737
37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | length:
| length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       %
Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-647-522-3
80
  BLOSUM62
Gapop 10.0 ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            June 10, 2002, 15:29:42 ; Search time 18.65 Seconds (without alignments) 31.142 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SwissProt_40:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105224 seqs, 38719550 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MSDGFYTMENSDRRK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20000000000
    GenCore
(c) 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gapext 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHIT_NPVOP
ESTE_MYZPE
RS6E_SULSO
LIPA_NEIMA
LIPA_NEIMB
FIBP_ADEB3
F16Q_BRANA
YNS7_YEAST
AROA_THEAC
YA12_SCHPO
POXB_ECOLI
IXA2_PHOLE
RECF_RICPR
GSHR_SCHPO
GSHR_SCHPO
MDBC_BP74
VGL2_IBVU
VGL2_IBVU
VGL2_IBVU
VGL2_IBVU
VGL2_IBVD
VGL2_IBVD
VGL2_IBVD
PGKA_CRIPA
FLIP_BORBH
FLIP_BORBH
FLIP_BORBH
FLIP_BORBH
FREL_CRIPA
FREL_CRIPA
FLIP_BORBH
FREL_CRIPA
FREL_CRIPA
FREL_CRIPA
FLIP_BORBH
FREL_CRIPA
FREL_CRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                version 4.5
- 2000 Compugen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105224
                      P30208
P17663
P52673
P12722
P11223
P112650
P044763
P44763
P25055
P11747
P11747
P4823
P32316
                                                                                                                                                                                                                                                                                                                            P29238
Q9zeb6
P78965
Q9y2q1
P07074
P30206
P30207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                6 avian infec
7 avian infec
8 avian infec
2 avian infec
2 avian infec
3 avian infec
3 avian infec
6 avian infec
6 avian infec
7 avian infec
7 saccharomyc
8 corynebacte
9 avian infec
                    rhizobium m
b aeropyrum p
b saccharomyc
                                                                                                                                                                                                                                                                                                                                                                       schizosacch
homo sapien
bacteriopha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 brassica na
3 saccharomyc
5 thermoplasm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neisseria
neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           myzus persi
sulfolobus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                schizosacch
escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     orgyia
                                                                                                                                                                                                                                                                                                                                                                                                                                     photobacter rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aden
```

SO S	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	888888888	RRA	RESULTION AC DT		•
HYC Enc SIC CHA CCAH CAH CAH CAH	EME Int Int Int PRO	Thire bet the use mod ent	[1] SEQ Ahr Roh "Th PO1 Vir	T_NPVOP CHIT_ O1036 01-NO 01-N	Ω :	35 35 35 36 37 38 38 38 38 44 44 44 46 46 46 46 46 46 46 46 46 46
POPLASE IOPLASE IOPLASE INAL IN LSITE BOHYD BOHYD BOHYD BOHYD BOHYD	POSTITE;	ils SWISS-P; tween the European be by non odified and tities req	QUENCE I DLINE-93 Tens C.I Drmann (De seque Lyhedro: COLOGY COLOGY COLOGY SUBCE SUBCE SIMIL HYDRO:	NPV 3; V-1 V-1 V-1 Die ble a p opo		35 35 33 33 33 33 35 35 35 35 35 35 35 35 35 3
Hydrolass; Glycosidase; Endoplasmic reticulum. SIGNAL 1 150 CARIN 17 550 ACT_SITE 304 304 CARBOHYD 146 146 CARBOHYD 172 172 CARBOHYD 172 172 CARBOHYD 344 344 SITE 547 550 SEQUENCE 550 AA; 6073	930; A/ 254; 10 1PR000 1PR000 1PR000 1PR000 0704; 0 00089; PS00014	(SS-PROT entry the Swiss IT pean Bioinfo non-profit and this sta a requires a an email to	727130C 727130C H., Rus G.F.; G.F.; ence of ence of 229:381 229:381 229:381 CASES).	7 (Re 7 (Re 7 (Re 7 (Re ndocl udot: udot: sDNA sDNA hedra	ω.	44444455.004444444444444444444444444444
Culum. 100 550 304 146 172 172 344 173 344 172 344 550	TN. 1579; C 1579; C 1679; C 1601; p 1601; p 1700_h PKD; 1 PKD; 1	entry is copyriss Institute of Sinformatics Institution in Statement is a license agricultulicense license agricultulicense license agricultulicense agricultul		TANDAF 35, 35, 11nase 1ruses 1ruses	42	
G. G. S.		is contitution nstitution cement	fed=91 ?.R., prgyia nome." 1997) 1997) 1997) 1997) 1997) 1997)	· re		7000000000
tin degrad	1. 6. 2	ght. It Bioinfo titute. ns as lo not remo eement (eement ()-sib.ch)	26251; Funk C.J., E Funk C.J., E pseudotsuga ; rolysis of t lymers of ch ndoplasmic r CHITINASE CI	PRT; ed) ed) sequence un annotation ursor (EC) apsid poly RNA stage;	NU5C_VICFA ALIGNMENTS	RN14_YEAST Y450_RHISN SYL_BUCAI RAS_ARTSA RS27_HALN1 HFLK_ECOLI YK27_CAEEL DNAA_RICPR ERG1_PANAN CT04 HIMAN
ation; Signal; L. ENDOCHITINASE DNOR (BY SIMIL, (GLCNAC) (GLCNAC) (GLCNAC) (GLCNAC) SECRETION FROM SCFP00E07BD CRC		produce atics a here are as its d. Usag e http:/	ans J., Ha a multinuc a multinuc e 1,4-beta tiin ticulum lu SS II (FAM	odate) update) s.2.1.14). hedrosis virus Baculoviridae	SI	
Glycopro ARITY). (POTENTI (POTENTI (POTENTI (POTENTI (POTENTI 64;		d through a nd the EMBL no restric content is by and forwards and forw	ood S., ocapsid inkages inkages	; (ОРИМФО)	595	P25298 P55656 P576262 P18262 Q9hrt7 P44546 P256666 Q16686 Q16686 Q186758
otein; AL). AL). AL). NTIAL).	•	collaborat outstatic tions on in no or commer .ch/annour		·	a faba	in sa a ny
		its way lal			:	និត្តិ ដើលជា មិន ទី

```
RESULT 2
ESTE_MYZPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                      Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1994
01-JUN-1994
01-OCT-1994
                                                                                                                                     CARBOHYD
CARBOHYD
                                                                                                       CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                     Hydrolase;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MECHANISM OF RESISTANCE TO ORGANOPHOSPHATE INSECTICIDES.
-1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)0 - an alocarboxylic antion
                                                                                                                                                                                                      DISULFID DISULFID
                                                                                                                                                                                                                                     ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institu
modified and this statement
entities requires a license
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myzus persicae (Peach-potato aphid).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha;
Aphidiformes; Aphidoidea; Aphididae; Macrosiphini; Myzus.
NCBI_TaxID-13164;
                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
PROSITE; PS00941; CARBOXYLESTERASE_B_2; FF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restitute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    resistance in the peach-potato aphid, Myzus Biochem. J. 294:569-574(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=R3 / ISOLATE 794J;
MEDLINE=93384534; PubMed=8373371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESTE_MYZPE P35501;
                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X74554; CAA52648.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Field L.M., Williamson M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Esterase E4
                                                                                                                                                                                                                                                                      ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning and analysis of the esterase
                                                                                                                                                                                                                                                                                                                                                                                          [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSDGFYTMENSDRRK 15
                                                                                                                                                                                                                                                                                                                                                                                                                        S36786; S36786.
; P21836; 1MAH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSDPFYFMHDADKRR 280
                                                                                                                                                                                                                                                                                                                                                                           PF00135;
                      Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                   IPR002018; Carboxylesterase_B.
IPR000379; Est_lip_thioest_actsite
                                                                                                                                                                                                                                                                                                                       Serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 29, Created)
(Rel. 29, Last sequence update)
(Rel. 30, Last annotation update)
precursor (EC 3.1.1.1) (Carboxylic-ester
                                                                                                                                                      24
214
339
463
463
89
266
81
269
371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                        Conservative
                                                                                                                                                                                                                                                                                                                                                                       COesterase;
                                                                                                       AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                       esterase;
                                                                                                                                      23
552
214
339
463
106
277
277
277
277
277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND SEQUENCE OF 794J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         license agreement
                                    53.8%;
                                                                                                       61348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53.8%;
46.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          institutions as long
                                                                                                       MW.
                                                                                                                  ESTERASE E4.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC.
                    Score 42; DB
Pred. No. 7.5;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is not removed.
                                                                                                                                                                                                                                                                                                                     Glycoprotein;
                      2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Moores G.D., Devonshire A.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                       B97B67272DFF7209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
                                                   DB
                                                                                                                                                                                                                                                                                                                                        FALSE_NEG
                                                                                                                                                                                                                                                                                                                     Signal.
                                                   ۳.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        persicae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         conferring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ω
--
                      4.
                                                  Length 552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 550
                                                                                                       CRC64;
                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                  (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        γd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hydrolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Sulzer).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IS A COMMON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        insecticide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alcohol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sı
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a collaboration
                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      outstation -
                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        way
                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                       ALD DE RESERVATION DE LA COMPANIA DEL COMPANIA DE LA COMPANIA DEL COMPANIA DE LA COMPANIA DEL CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
RS6E_SULSO
      RRN OCC OCC DIT
                                                                                                                                                                                                                                                                                                                   Ş
                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QΥ
                                                                                                                                                                                                                    LIPA_NEIMA
                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 7
                                                                                                                                 LIPA_NEIMA STANDARD;
p57037;
p57037;
l6-OCT-2001 (Rel. 40, Last seg
l6-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A., De Moors A., Erauso G., Fletcher C., Gordon P.M.K., Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N. Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T., Carrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.; "The complete genome of the crenarchaeon Sulfolobus Solfataricus Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
SEQUENCE FROM N.A. STRAIN-22491 / SEROGROUP A / SEROTYPE 4A;
                                                                                                    Capsule polysaccharide LIPA OR NMA0186.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01092; Ribosomal_S6e; 1.
ProDom; PD003460; Ribosomal_S6E;
PROSITE; PS00578; RIBOSOMAL_S6E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Extreme Bioinformatics Institute. There are no restricted the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     She Q., Singh
                                                                 Neisseria meningitidis (serogroup
Bacteria; Proteobacteria; beta sul
                                                                                                                                                                                                                                                                                                                                                                                                                                       Ribosomal protein; SEQUENCE 214 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE006674; AAK40739.1; -. InterPro; IPR001377; Ribosomal_S6E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-ATCC 35092 / DSM 1617 / P2;
MEDLINE-21332296; PubMed-11427726;
She Q., Singh R.K., Confalonieri F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sulfolobus solfataricus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RPS6E OR SSO041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q980A6;
                                                  NCBI_TaxID=65699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archaea; Crenarchaeota;
NCBI_TaxID=2287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RS6E_SULSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
                                                                                                                                                                                                                                                                                    182 GFYPNENGERRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            474 DGFYVYDNEEDRK 486
                                                                                                                                                                                                                                                                                                     4 GFYTMENSDRRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DGFYTMENSDRRK
                                                                                                                                                                                                                                                                                                                                                  Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     non-profit institu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel.
(Rel.
                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                     15
                                                                                                                                                                                                                                                                                        193
                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete p
23720 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      institutions as long atement is not removed.
                                                                                                                                                                                                                                                                                                                                                                     58
                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last annotation S6e.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last
                                                                                                                   modification protein
                                                                                                                                                                                                                                                                                                                                                                  3 %;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sulfolobales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence
                                                                                                                                                                                                                                                                                                                                                      2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     proteome
                                                                                                                                                                                                                                                                                                                                                    Score 41; DB Pred. No. 4.1; 2; Mismatches
                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                 sup A).
subdivision; Neisseriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                     9E20B93EB0247693 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zivanovic Y., Allard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           214
                                                                                                                                                                                                   704
                                                                                                                                                                                                                                                                                                                                                                    DB
4.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sulfolobaceae; Sulfolobus
                                                                                                                                                                                                     ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as its content
                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                   lipA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Usage
                                                                                                                                                                                                                                                                                                                                                      ω
``
                                                                                                                                                                                                                                                                                                                                                                                   Length 214
```

γģ

for

commercia:

.ch/announce/

restrictions and

EMBL

a collaboration

outstation

solfataricus P2.";

G.

Indels

0,

Gaps

0

Neisseria

```
RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ρy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Best I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                             LIPA_NEIMB
Q05013;
Q1-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Ratherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G., Wartell B.G., Gorphiete DNA sequence of a serogroup A strain of Neisseria
                                                                                                                   Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson Elsen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty I Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.; "Complete genome sequence of Neisseria meningitidis serogroup B:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             meningitidis Z2491.";
Nature 404:502-506(2000).
-i- FUNCTION: INVOLVED IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                       NEIMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the
                                                                                                         MC58,
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-MC58 / SEROGROUP B;
MEDLINE-20175755; PubMed-10710307;
                                                                                                                                                                                                                                                                                                                                                       Capsule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20222556;
Parkhill J., Achtr
                                    STRAIN=B1940 / SEROGROUP B;
MEDLINE=93316845; PubMed=8326861;
                                                                                                                                                                                                                                                                                                                            Neisseria
                                                                                                                                                                                                                                                                                                                                       Capsule polysaccharide LIPA OR NMB0082.
               "Phospholipid substitution
                          Frosch M., Mueller
                                                     SEQUENCE OF 184-704 FROM STRAIN=B1940 / SEROGROUP
                                                                                          Science
                                                                                                                                                                                                                                                                                                NCBI_TaxID=491;
                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G
 capsule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ween the Swiss Institute of Bioinfo
European Bioinformatics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSLOCATION TO THE CELL SUBCELLULAR LOCATION: INNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIDE) (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAPSULAR POLYSACCHARIDE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a centre Swiss Institute of Bioinformatics and the EMBL Eduropean Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDGFYTMENSDRRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDGLQSINNNNRRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL162752;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 7; Conserv
                                                                                            287:1809-1815(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteome.
704 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           non-profit institutions as long and this statement is not removed.
                                                                                                                                                                                                                                                                                                                            meningitidis
                                                                                                                                                                                                                                                                                                                                                                  (Rel. 30,
(Rel. 40,
(Rel. 40,
 formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAB83501.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polysaccharide transport; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=10761919;
man M., James K.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50
50
 in
                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
e modification protein 1
                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                              (serogroup B).
.a; beta subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .0%;
 Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INNER MEMBRANE-ASSOCIATED (CYTOPLASMIC
of capsular polysaccharides isseria meningitidis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHOSPHOLIPID MODIFICATION OF A STRONG REQUIREMENT FOR ITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2E1C5DE665D9BB61 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bentley
                                                                                                                                                                                                                                                                                                                                                                                                                        704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                               Neisseriaceae; Neisseria
                                                                                                                                                                                                                                                                                                                                                       lipA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ω,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             γď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      restrictions
               and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      collaboration
                                                                                                                                                                           E.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                         B
                                                                                                                         strain
                                                                                                                                                                                                                               7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŝ
                                                                                                                                                                                        .A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                               .
[7]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
```

В ş

Ģ

SDGLQSINNNNRRK

18 15

2 SDGFYTMENSDRRK

FIBP_ADEB3 RESULT

FIBP_ADEB3

STANDARD;

PRT;

976

A

RRITARY RAY

SEQUENCE FROM N.A. MEDLINE=93107871;

Bovine adenovirus type Viruses; dsDNA viruses,

no

(Mastadenovirus bos3). no RNA stage; Adenoviridae;

Mastadenovirus.

NCBI_TaxID=10510;

01-OCT-1994 15-DEC-1998 Q03553; 01-OCT-1993

(Rel. (Rel. (Rel.

27, Created)
30, Last sequal
37, Last anno

sequence update)
annotation update)

Fiber

protein.

Mittal S.K., Prevec L., Babiuk L.A., Gr. "Sequence analysis of bovine adenovirus

Graham

type

ı F.L.; be 3 ea

early

region

w

PubMed=1469367;

Mittal S.K., Prevec L., Babiuk L.A., Gri "Sequence analysis of bovine adenovirus fibre protein genes.";

Graham

type

n F.L.; e 3 ea

early

region

Gen.

Virol.

genes."; . 74:2825-2825(1993)

MEDLINE=94103794; PubMed=8277294; Mittal S.K., Prevec L., Babiuk L.

REVISIONS

ibre Gen.

protein genes n. Virol. 73:33

73:3295-3300(1992)

```
SO TITITIES TO BE SO TO THE TITIES OF THE TI
Matches
                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i-
                                                                                                                                                   CONFLICT
SEQUENCE
                                                                                                                                                                                                                                        CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE002367; AAF40546.1; -.
EMBL; Z13995; -; NOT_ANNOTATED_CDS
PIR; S28077; S28077.
PIR; S32879; S32879.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inner membrane; Polysaccharide Complete proteome.
CONFLICT 238 238 • H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between
                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                                                               CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  European Bioinformatics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSLOCATION TO THE CELL SURFACE.
SUBCELLULAR LOCATION: INNER MEMBRANE-ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAUTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                566 ONWARD DUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAPSULAR POLYSACCHARIDE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a deen the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Microbiol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NMB0082; -
Similarity 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PROBABLE)
                                                                                                                                                      704
                                                                                                                                                                                  238
2294
206
316
316
331
449
456
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REF.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INVOLVED IN THE
                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8:483-493(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TO A FRAMESHIFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                  238
2253
2297
2306
3316
331
449
456
                                                                                                                                                      79605
                               50.0%;
                                                                                                                                                         MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIFFERS FROM THAT SHOWN
   4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A STRONG
                                                                                                                                                                                  Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                    < ≖
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHOLIPID MODIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                 ٠ '
                                                                                                                                                         2909C40642CD326A
   Mismatches
                                                                                                                                                                                                                                              ខាងងក
                                  No.
                                                           40;
                                                                                                                                                                                  > KIDS (IN REF. 1 (IN 
                                                                                                                                                                                                                                                                                                                                                                                                                          NI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REQUIREMENT
                            DB
22;
                                                                                                                                                                                                                                                                                                                                                                                                                                 REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Usage
                                                                                                                                                                                                                                                                                                                                                                                                    REF.
   ω,
                                                              Length 704;
                                                                                                                                                         CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FOR
      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ϋ́
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POSITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for
   0;
      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                n no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               no
      0
```

```
RESULT 7
                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : TISSUE-Cotyledon;

K MEDLIKE-95357438; PubMed-7630967;

K Laroche A., Frick M.M., Kazala C., Weselake R.J., Thoma I Isolation and characterization of an oilseed rape fruc I bisphosphatase cDNA.";

L Plant Physiol. 108:1335-1336(1995).

C -! CATALYTIC ACTIVITY: D-Tructose 1.6-bisphosphate + H fructose 6-phosphate + phosphate.

C -! SUBCELLANEOUS: IN PLANTS THERE ARE TWO FBPASE ISOZY CYTOSOL AND THE OTHER IN THE CHLOROPLAST.

C -!- SIMILARITY: BELONGS TO THE FBPASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; D16839; BAA04115.1; -.
EMBL; AF030154; AAD09736.1; -.
Interpro; IPR000939; Adeno_fiber2.
Interpro; IPR000978; Adeno_fiber_knob.
Interpro; IPR000931; Adeno_fibre.
Pfam; PF00541; adeno_fiber; 1.
Pfam; PF00541; adeno_fiber2; 16.
PFINTS; PR00307; ADENOVSFIBRE.
                                                                                                                                                                                                                                                                                      bispnospunce (Rape).
Brassica napus (Rape).
Bukaryota; Viridiplantae; Streptophyta; Embryo
Eukaryota; Viridiplantae; eudicotyledons;
Mannoliophyta; eudicotyledons;
Brass
                                                                                                                                                                                                                                                                                                                                01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Fructose-1,6-bisphosphatase, cytosolic (EC 3.1.
bisphosphate 1-phosphohydrolase) (FBPase)
                                                                                                                                                                                                                                                                                                                                                                                                                      F160_BRANA
P46267;
                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
           between the the European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- FUNCTION: RECOGNIZES THE CELL RECEPTOR;
BETWEEN THE ADENOVIRUS CAPSID AND THE H
-i- SUBUNIT: HOMOTRIMER.
                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bovine adenovirus type 3.";
J. Virol. 72:1394-1402(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98105785; PubMed=9445040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-WBR-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Nucleotide sequence, genome organization,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MSDGLYTKDN 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MSDGFYTMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Babiuk L.A., Tikoo S.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      976 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Idamakanti
                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102323 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zakhartchouk A.N.,
           Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9D0EC36052F02896 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No.
                                                                                                                                                                                                                                                                                                                                                                                                                                   339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31.
        There
                                                                                                                                                                                                                                                                                                              Embryophyta;
                                                                                                                                                                                                                                                                                        Brassica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                   B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HOST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SERVES AS THE LI
and and a
                                                                                                                                                                                                                                                                                                  core
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baxi M.K.,
                                                                                                                                                                                                                                                                                                                                                              'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transcription map of
                                                                                                                                                                                                                                                                                                                                                           .11)
                                                                                                                                                                                Thomas J.E.;
e fructose-1,6-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                              ISOZYMES: ONE
                                                                                                                                                                                                                                                                                                    eudicots;
                                                                                                                                        +
                                                                                                                                                                                                                                                                                                                Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                           (D-fructose-1,
           restrictions
                                                                                                                                      H(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THE LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lee J.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                              IN THE
           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
```

```
RESULT 8
YNS7_YEAST
ID YNS7_Y
  Вþ
                                               Š
                                                                                                                                                                                                                                              A PROCECCIO COCCEPA PROCECCIO COCCECCIO COCCEPA PROCECCIO COCCEPA PROCECCIO COCCEPA PROCECCIO COCCECCIO COCCEPA PROCECCIO COCCEPA PROCECCIO COCCEPA PROCECCIO COCCECCIO COCCEPA PROCECCIO COCCECCIO COCCENTE PROCECCIO COCCECCIO COCCECCIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qy
                                                                                                      Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P53873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Obermaier
Submitted
                                                                                                                                                                                                                                         EMBL; Z71463; CAA96081.1; -. SGD; S0005131; YNL187W. Hypothetical protein. SEQUENCE 357 AA; 40307 MW
                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last seq
15-JUL-1998 (Rel. 36, Last ann
Hypothetical 40.3 kDa protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00316; FBPase; 1.

PRINTS; PR00377; INFBPHPHTASE.

PRODOM; PD001491; In_FB_phphtase; 1.

PROSTIE; PS00124; FBPASE; 1.

Hydrolase; Carbohydrate metabolism; Multigene family.

ACT_SITE 276 276 BY SIMILARITY

ACT_SITE 339 AA; 37156 MW; 3844CD90F3C6DD33 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                         entities requires
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM Obermaier B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U20179; AAA82750.1;
HSSP; P00637; 1BK4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000146; In_FB_phphtase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NL187W OR N1615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139 GIYTMEHSD 147
  65
                                            3 DGFYTM--ENSDR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 GFYTMENSD 12
DPFYTLYNENSDR
                                                                                                      similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FROM N.A.

B., Piravandi E., Rinke M., Domdey H.;
(MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                         license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48.8%;
77.8%;
                                                                                                                               48.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
protein in KAR1-UBP10 i
                                                                                                                                                                                                                                              ¥.
                                                                                                      Score 39; DB Pred. No. 16; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 39; DB Pred. No. 15; 1; Mismatches
                                                                                                                                                                                                                                           ED52B00C4902453A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      357
                                                                                                                                                                                                                                                                                                                                                                                              (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
15;
                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . Usage by and for commercial http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    intergenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  its content
                                                                                                                                                           Length 357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a collaboration - MBL outstation
                                                                                                      2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'n
                                                                                                                                                                                                                                                                                                                                                                                                                                  commerci
                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ņ
                                                                                                                                                                                                                                                                                                                                                                                                                                                      way
                                                                                                      1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
```

AROA_THEAC
ID AROA_THEAC
AC Q9HLE6;
DT 16-OCT-2001
DT 16-OCT-2001

STANDARD;

PRT;

410

Q9HLE6; 16-OCT-2001 16-OCT-2001

(Rel.

40,

Last Created)

sequence update)

RESULT

```
20
밁
                                                                                                                                                                                                                                                                                                                                                                                               Query
Best L
                                                                                                                                                                 009685;
01-NOV-1995 (Rel. 3
01-NOV-1995 (Rel. 3
16-OCT-2001 (Rel. 4
Hypothetical 48.5 k
SPAC13C5.02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AL445063; CAC11427.1; -.
Interpro; IPR001986; EPSP_Syntase.
Pfam; PF00275; EPSP_Syntase; 1.
ProDom; PD001867; EPSP_Syntase; 1.
PROSITE; PS00104; EPSP_SYNTHASE_1; FALSE_NEG.
PROSITE; PS00885; EPSP_SYNTHASE_2; FALSE_NEG.
Aromatic amino acid biosynthesis; Transferase; Complete SEQUENCE 410 AA; 45166 MW; 0EF167698CC2FA26 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIJINE-20479972; PubMed-11029001;
Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K.,
Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeis
"The genome sequence of the thermoacidophilic scavenger T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thermoplasma acidophilum.
                                                                                                                                                                                                                                                                   SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acidophilum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Last annotation update)
Probable 3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19)
(5-enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase) (EPSPS).
AROA OR TA0282.
           Devlin K., Churcher C.M., Ba
Submitted (JUL-1995) to the
-!- SIMILARITY: CONTAINS 2 W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 407:508-513(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=DSM 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=2303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified
                                                    STRAIN-972;
                                                                                             NCBI_TaxID=4896
                                                                                                                         Schizosaccharomycetales;
                                                                                                                                        Eukaryota; Fungi;
                                                                                                                                                  Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                            136
                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                        ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate phosphate + 5-0-(1-carboxyvIny1)-3-phosphoshikimate.
PATHWAY: SIXYH STEP IN THE BIOSXNYHESIS OF CHORISMATE WITHIN BIOSXNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: MONOMER (BY SIMILARITY).
SUBCELLULAR LOCATION: Cytoplasmic (Probable)
                                                                                                                                                                                                                                                                                                                           DGFYDVDGSESKK 148
                                                                                                                                                                                                                                                                                                                                                      DGFYTMENSDRRK
                                                                                                                                                                                                                                                      SCHPO
                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            non-profit institutions as long as its content is in no way and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                               32,
32,
40,
kDa
                                                                                                                                         Ascomycota;
                                                                                                                                                                                                                                                                                                                                                      15
                                                                                                                                                                                                                                                                                                                                                                                               46
                                                                                                                                                                            Last sequence update)
Last annotation updat
protein C13C5.02 in c
                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                               . 88
                                                                                                                         Schizosaccharomycetaceae;
          Barrell B.G., Rajandhe EMBL/GenBank/DDBJ WW DOMAINS.
                                                                                                                                                     (Fission yeast)
                                                                                                                                                                                                                                                                                                                                                                                               Score 39; DB Pred. No. 18;
                                                                                                                                        Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPSP SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                      411
                                                                                                                                                                               update)
2 in chromosome
                                         Rajandream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermoplasmaceae;
                                                                                                                                                                                                                                                      A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           here are no restrict
as its content is
                                                                                                                                                                                                                                                                                                                                                                                                             1;
                          databases
                                                                                                                                                                                                                                                                                                                                                                                                             Length 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Baumeister W.;
                                         M.A.,
                                                                                                                                                                                 H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thermoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Volker C.,
                                         Walsh
                                                                                                                                                                                                                                                                                                                                                                                  0,
                                       s.v.;
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                  0;
```

```
RESULT
POXB_EC
В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01846; FF; 1.
Pfam; PF00397; WW; 2.
PRINTS; PR00403; WMDOMAIN.
SMART; SM00441; FF; 1.
SMART; SM00456; WW; 2.
                                                                                                                                                                                                                                                                                                                                                    01-APR-1988
01-APR-1988
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
InterPro;
InterPro;
                                                        Science [3]
                                                                               Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A. Book Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein;
DOMAIN 3
DOMAIN 89 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          esu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z50112; CAA90453.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified
MEDLINE~97061202; PubMed~8905232; Oshima T., Aiba H., Baba T., Fujita Ikemoto K., Inada T., Itoh T., Kajil
                                                                                                                     SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, B
                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Last annotation update)
Pyruvate dehydrogenase [cytochrome] (EC 1.2.2
(POX) (Pyruvate dehydrogenase [Ubiquinone]).
                                                                                                                                                                                                                                                                                                                                                                                                                         ECOLI
                                                                                                                                                                            "Nucleotide sequence and deduced amino acid sequence of Escherichia coli pyruvate oxidase, a lipid-activated flavoprotein."; nucleic Acids Res. 14:5449-5460(1986).
                                  STRAINEK
                                             SEQUENCE
                                                                 "The complete genome sequence Science 277:1453-1474(1997).
                                                                                                                                                                                                                 Grabau C.,
                                                                                                                                                                                                                          MEDLINE=86286555; PubMed=3016647;
                                                                                                                                                                                                                                       STRAIN-K12;
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                       NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                    Escherichia
                                                                                                                                                                                                                                                                                               Bacteria;
                                                                                                                                                                                                                                                                                                         Escherichia
                                                                                                                                                                                                                                                                                                                    POXB OR B0871
                                                                                                                                                                                                                                                                                                                                                                                                P07003; Q47513;
                                                                                                                                                                                                                                                                                                                                                                                                            POXB_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DRFYVLDSGERRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DGFYTMENSDRRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS01159; WW_DOMAIN_1;
PS50020; WW_DOMAIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              non-profit institutions as long and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR002713;
IPR001202;
                                           FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR002349;
                                                                                                                                                                                                                                                                                             Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89
411 AA;
                                                                                                                                                                                                               Cronan J.E.
                                                                                                                                                                                                                                                                                                                                                    (Rel. 07, Last sequence up
(Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                           coli.
                                                                                                                                                                                                                                                                                                                                                                          (Rel. 07, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                               STANDARD; ; Q47514; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 W
122 W
; 48519 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15
                                                                                                                                                                                                                                                 AND PARTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WW_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 88;
                                                                                                                                                                                                                                                                                                                                                                                                   Q47515;
                                                                                                                                                                                                                                                                                              gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M M
                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                            of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                RT; 572
Q47516; Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7A89C5F7397B8AAF CRC64;
                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                               subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39;
No.
          Χ.,
                                                                                                                                                                                                                                                                                                                                                               update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                 Q47517;
Hayashi K., H
M., Kanai K.,
                                                                                                                                                                                                                                                                                                                                                                                                            3
                                                                                                                                                                                                                                                                                                                                           .2.2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Usage
                                                                                                                                                                                                                                                                                                Enterobacteriaceae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 411
                                                                                                                                                                                                                                                                                                                                                                                                   Q47518; Q47519;
                                                                                                                                                                                                                                                                                                                                          (Pyruvate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Λq
           Hon jo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and
                                                                                                                                                                                                                                                                                                                                             oxidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
```

Kajihara

Kashimoto

```
ECO2DBASE; GOS8 0; 6TH EDITION.
ECOGene; EG10754; pox8.
InterPro; IPR00309; TPP_enzyme.
Pfam; PF00205; TPP_enzymes; 1.
Pfam; PF02775; TPP_enzymes_C; 1.
Pfam; PF02776; TPP_enzymes_N; 1.
PfAm; PF02776; TPP_enzymes_N; 1.
Ox1doreductase; Flavoprotein; FAD; T.
Ox1doreductase; Flavoprotein; FAD; T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kimura S., Kitagawa M., Makino N. Moroi H., Mocomura K., Nakamura Y. Sampei G., Seki Y., Tagami H., Ta Yano M., Horiuchi T.;
"A 718-kb DNA sequence of the Esc corresponding to the 12.7-28.0 m." DNA Res. 3:137-155(1996).
                                                                                                      HSSP; P37063;
SWISS-2DPAGE;
ECO2DBASE; G05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Grabau
"Lipid
                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 550-572 FROM N.A. MEDLIND-86033917; PubMed-3902830; Recny M.A., Grabau C., Cronan J.E. Jr., "Characterization of the alpha-peptide activation of pyruvate oxidase."; J. Biol. Chem. 260:14287-14291(1985).
                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a cetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chang Y.Y., Wang A.Y., Cronan J.E. Jr.;
"Expression of Escherichia coli pyruvate oxidase (P
the sigma factor encoded by the rpoS(katF) gene.";
Mol. Microbiol 11:1019-1028(1994)
-i- CATALYTIC ACTIVITY: Pyruvate + ferricytochrome
+ acetate + ferrocytochrome b1.
-i- COFACTOR: THIAMINE PYROPHOSPHATE, FAD AND MAGNE
                                                                                                                                                        EMBL;
                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-22 FROM N.A. MEDLINE-94293772; PubMed=8022274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biol.
                                                                                                                                                                     EMBL;
                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-89308683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u></u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S
                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: HOMOTETRAMER.
SUBCELULAR LOCATION: Membrane-associated.
SUBCELULAR LOCATION: Membrane-associated.
PTM: ACTIVATED BY LIMITED PROTEOLYTIC DIGESTION. THIS CLEAVAGE PTM: ACTIVATED BY LIMITED PROTEOLYTIC DIGESTION OF ENDUCES A PEPTIDE (ALPHA-PEPTIDE) AND MIMICS THE ACTIVATION OF ENZYME BY PHOSPHOLIPIDS. THE PROTEOLYTIC CLEAVAGE ALSO RESULTS I THE LOSS OF THE HIGH AFFINITY LIPID-BINDING SITE OF THE ENZYME.
SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.
                                                                                                                                        ; L47694; AAB59108
; L47695; AAB59109
A23648; DEECPC.
                                                                                                                                                     X04105; CA
AE00724; BA
D90724; BA
S73268; AA
M28208; AA
L47689; AA
L47690; AA
L47691; AA
L47692; AA
L47693; AA
L47693; AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               u C., Chang Y.Y., Cronan J.E. Jr.; d binding by Escherichia coli pyruvate alterations of the carboxyl-terminal ol. Chem. 264:12510-12519(1989).
                                                                                                                                                                                                                                                                                                                                                                           non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FROM N.A.,
                                                                                                                                                    P07003; COLI.
58.0; 6TH EDITION.
                                                                                                                                                                                                                                                                                                            CAA27725.1;
                                                                                                                               1POW
                                                                                                                                                                                                                                                                                                 AAC73958.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=2663858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AND MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   o K., Masuda S.
a Y., Nashimoto
, Takemoto K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli K-12 genome map.";
  proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jr.,
           Thiamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pyruvate oxidase is disrupted
terminal region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Masuda S.,
Nashimoto
                                                                                                                                                                                                                                                                                                                                               (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                    There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  released upon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hager L.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     о н.,
Wada
           pyrophosphate; Magnesium,
                                                                                                                                                                                                                                                                                                                                                             Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAGNESIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Miki T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nishio
1 C., Yam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PoxB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       b1
+
                                                                                                                                                                                                                                                                                                                                                             bу
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hio Y., Saito
Yamamoto Y.,
                                                                                                                                                                                                                                                                                                                                                                                    restricti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mizobuchi K.,
                                                                                                                                                                                                                                                                                                                                                             and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H(2)0 =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            depends
                                                                                                                                                                                                                                                                                                                                                                                                            collaboration
                                                                                                                                                                                                                                                                                                                                                                                                 outstation
                                                                                                                                                                                                                                                                                                                                                                         in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                H
                                                                                                                                                                                                                                                                                                                                                                         no
                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                        way
```

```
ALD DON'S STANDARD CONTRACTOR OF THE STANDARD CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P29238;
01-DEC-1992
01-DEC-1992
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _PHOLE
LXA2_PHOLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-ATCC 25521;
MEDLINE-92007870; PubMed-1915359;
MEDLINE-92007870; PubMed-1915359;
Lee C.Y., Szittner R.B., Meighen E.A.;
"The lux genes of the luminous bacterial symbiont, Photo leiognathi, of the ponyfish. Nucleotide sequence, differ organization, and hish expression in mutant Escherichia Eur. J. Biochem. 201:161-167(1991).
-!- FUNCTION: LIGHT-EMITTING REACTION IN LUMINOUS BACTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEPTIDE
ACT_SITE
MUTAGEN
     DOMAIN
                                                                                                                        InterPro; IPR002103; Bac_luciferase
Pfam; PF00296; bac_luciferase; 1.
                                                                                                                                                               EMBL; M63594; AAA25618.1; PIR; S17953; S17953. HSSP; P07740; 1LUC.
                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MUTAGEN
MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MUTAGEN
MUTAGEN
                                       DOMAIN
                                                    Photoprotein; Luminescence; Flavoprotein; FMN.
                                                                     PROSITE; PS00494; BACTERIAL_LUCIFERASE; 1.
Photoprotein; Luminescence; Oxidoreductase;
                                                                                                                                                                                                                                                                                                                the
                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. between the Swiss Institute of Bio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Photobacterium leiognathi.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alkanal monooxygenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Photobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lpha chain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N
                                                                                                                                                                                                                                                                                                            ween the Swiss Institute of Bioinf
European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                         light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSGFHTMMNAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDGFYTMENSD
                                                                                                           PR00089; LUCIFERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 63.7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel.
(Rel.
     279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            550
553
553
553
553
572
                                       100
                                                                                                                                                                                                                                                                                                                                                                                    HETERODIMER OF AN ALPHA AND A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24,
24,
40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          572
572
572
365
416
62011
                                       115
     294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .89
                                                                                                                                                                                                                                                                                                                                                                                                                  TTING REACTION IN LUMINOUS BACTERIA RCHO' + FMNH(2) + O(2) - RCOOH + FM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALPHA-PEPTIDE.
BY SIMILARITY.
A->T: IN POXB11.
A->V: IN POXB14. NORMAL ACTIVI'
E->P: IN POXB16; NORMAL ACTIVI'
R->G: IN POXB10; REDUCED ACITIVI'
R->G: IN POXB10; REDUCED ACITITI'
INTERACT LESS WITH MEMBRANES.
MISSING: IN POXB6.
MISSING: IN POXB8.
MISSING: IN POXB8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score Pred 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2
                  REGION OF ACTIVE SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QQ -> HE (IN REF. 4).
QAL -> HGV (IN REF. 4).
; 57B38B9E3A92BDEA CRC64;
                                                                                                                                                                                                                                                                                                                               Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No.
   ę
                                                                                                                                                                                                                                                                                                                                            It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26;
                                                                                                                                                                                                                                                                                      There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                    http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                    BETA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ۲.
                                                                     Monooxygenase;
                                                                                                                                                                                                                                                                       Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vibrionaceae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
ພ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOSS OF ACTIVITY. REDUCED ACITIVITY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 572;
                                                                                                                                                                                                                                                                                                                             and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Bacterial luciferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          difference
richia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Photobacterium
                                                                                                                                                                                                                                                                           γď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTIVITY
                                                                                                                                                                                                                                                                                                          restrictions
(BY
                                   (BY
                                                                                                                                                                                                                                                                           and
                                                                                                                                                                                                                                                                                                                                                                                                                        FMN
                                                                                                                                                                                                                                                                                           S
                                                                                                                                                                                                                                                                                                                                                ۵
                                                                                                                                                                                                                                                                                                                                                                                                                        +
                                                                                                                                                                                                                                                                           ioi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                 collaboration -
L outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ...
:: 5
                                                                                                                                                                                                                                                                                                         outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                      H(2)0
                                                                                                                                                                                                                                                                                           'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                         commercia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAY
                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                          way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
```

```
RESULT 14
GSHR_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
RECF_RI
                                                                  Вb
                                                                                              Š
                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                  Matches
                                                                                                                                                                                                                   NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-99039499; PubMed-9823893;
Andersson S.G.E., Zomorodipour A., Andersson J.O.,
Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M.,
Eriksson A.-S., Winkler H.H., Kurland C.G.;
"The genome sequence of Rickettsia prowazekii and th
mitochondria.";
                                                                                                                                                                                                                                                            EMBL; AJ235270; CAAA14500.1; -.
InterPro; IPR001238; RecF.
Pfam; PF00470; RecF; 1.
PROSITE; PS00617; RECF_1; 1.
PROSITE; PS00618; RECF_2; 1.
DNA damage; DNA replication; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 396:133-140(1998).

-1- FUNCTION: THE RECF PROTEIN IS INVOLVED IN DNA METABOLISM: IT IS
-1- FUNCTION: THE RECF PROTEIN AND NORMAL SOS INDUCIBILITY. RECF
BINDS PREFERENTIALLY TO SINGLE-STRANDED, LINEAR DNA. IT ALSO SEEMS
TO BIND ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA replication and repair RECF OR RP029.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RECF_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM
STRAIN=MADRID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rickettsiaceae;
NCBI_TaxID=782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9ZEB6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RICPR
                                                                                                                                                                                                                                                ATP-binding;
                                                                 125 EGIFTSSSTDRRK 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  w
                                                                                                 ω
                                                                                                                                                                                                                                                                                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through a collaboration went the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE RECF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RICPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DGFYTMEN 10
                                                                                                 DGFYTMENSDRRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DGFYTLEH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 6; Conser
                                                                                                                                  Similarity 6; Conser
                                                                                                                                                                                                                   360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prowazekii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                    Complete proteome
33 40 A
                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rickettsieae;
                                                                                                 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40402 MW;
                                                                                                                                                                                                                   41489 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47.5%;
75.0%;
                                                                                                                                                 47
                                                                                                                                                . 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
                                                                                                                                  4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>ب</u>
                                                                                                                                Score 38; DB
Pred. No. 24;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 38; DB Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY).
; 07001C2064F4645B CRC64;
                                                                                                                                                                                                                 ATP (POTENTIAL).
; S00B37B88D77A16D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                recF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
                                                                                                                                                 DB
24;
                                                                                                                                                                                                                                                                                                                                                                                                                             There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B
                                                                                                                                                                                                                                                                 SOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                 Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 354
                                                                                                                                                                                                                                                                 response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                               Length 360
                                                                                                                                                                                                                   CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the origin
                                                                                                                                                                                                                                                                                                                                                                                                                 Ьy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Naeslund
                                                                                                                                                                                                                                                                                                                                                                                                                 and
                                                                                                                                                                                                                                                                 DNA repair;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                   tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                Gaps
                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
 InterPro; IPR001327; EINTERPro; IPR000815; FINTERPro; IPR000205; NINTERPRO; IPR000103; FINTERPRO; F
                                                                                                                                                                                                                                                                                                                                                                                entities
or send a
                              NP_BIND
DISULFID
                                                                                                                                                                                                                                                                                                 EMBL;
HSSP;
NP_BIND
ACT_SITE
                                                                                                                                                          InterPro; IPR004099; pyr_redox_dim.
Pfam; PF00070; pyr_redox; 1.
Pfam; PF02852; pyr_redox_dim; 1.
DBIND; PF02852; pyr_redox_dim; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- CATALYTIC
                                                                 Redox-active
                                                                                  PROSITE;
                                                                                                                                                                                                                 InterPro; IPR001100;
                                                                                                          I; PF02852; pyr_redox_d1
VTS; PR00368; FADPNR.
VTS; PR00945; HGRDTASE.
VTS; PR00411; PNDRDTASEJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glutathione
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOSOL
                                                                                                                                                                                                                                                                                                P00390; 1ALG.
                                                                                              PR00411; PNDRDTASEI.
PR00469; PNDRDTASEII
46
305
453
                                                                 center;
```

er; Oxidoreductase; IFAD (ADP)
39 FAD (ADP)
51 REDOX-ACT
315 FAD (FLAN
453 BY SIMILA

FAD (ADP PART) (PROBABLE).

REDOX-ACTIVE (BY SIMILARITY).

FAD (FLAVIN PART) (BY STATIONARY).

BY SIMILAPTET:

(BY SIMILARITY)

PYRIDINE_REDOX_1; 1

pyr_redox. Pyridine_redox_2. NAD_binding. FAD_pyr_redox

```
GSHR_SCHPO STANDARD; PRT; 464
P78965; 013631;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence upda
01-MAR-2002 (Rel. 41, Last annotation up
Glutathione reductase (EC 1.6.4.2) (GR)
PGRI OR SPBC17A3.07 OR P1039.
                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Isolation, expression, and regulation of glutathione reductase absolutely required Schizosaccharomyces pombe.",
J. Biol. Chem. 272:23042-23049(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wood V., Skelton J., Submitted (JUL-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kushida N., Yamazaki S., Tanaka T., Jinno K., Halkawa Y., Ya
Yamamoto S., Sekine M., Oguchi A., Nagai Y., Sakai M., Aoki
Ogura K., Otsuka R., Kudoh Y., Yanagida M., Machida M., Zhar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomyces pombe (Fission Eukaryota; Fungi; Ascomycota; Schiz
                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ogura K., Otsuka R., Kuć
Submitted (MAY-1997) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-97435263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schizosaccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      d V., Skelton J., Churcher C.M., Rajandream M.A., Barrell B.G. mitted (JUL-1999) to the EMBL/GenBank/DDBJ databases. FUNCTION: MAINTAIN HIGH LEVELS OF REDUCED GLUTATHIONE IN THE
                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Cytoplasmic MISCELLANEOUS: THE ACTIVE SITE IS
                                                                                                                                                                                                                                                                                                OXIDOREDUCTASES CLASS-I.
                                                                                                                                                                                                                                                                                                                                                                                               COFACTOR: FAD (BY SIMILARITY)
U63845; AAC49809.1; -. AB004537; BAA21419.1; AL109652; CAB51766.1;
                                                                                                 s requires a license agreement (S an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dawes I.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTIVITY: NADPH + oxidized glutathione =
                                                                                                                                                                                                                                                                                                                  LOCATION: Cytoplasmic (By similarity).
US: THE ACTIVE SITE IS A REDOX-ACTIVE DISULFIDE BELONGS TO THE PYRIDINE NUCLEOTIDE-DISULFIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=9287302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roe J.-H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GR) (GRase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        464
                                                                                                                          (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
                                                                                                                                                                                          There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ×.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for
                                                                                                                                                                        as its content
                                                                                                                        http://www.isb-sib
                                                                                                                                               Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pgr1(+) gene encoding
the growth of
                                                                                                                                                 уд
                                                                                                                                                                                               restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                               NADP(+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhang M.Q.;
                                                                                                                                                                                                                           EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamazaki J.,
                                                                                                                                                                                                                                                  a collaboration
                                                                                                                                               for
                                                                                                                                                                                                                                                                                                                                                 BOND
                                                                                                                                               commercial
                                                                                                                                                                                                    9
```

```
RESSOLITE RESOLUTION OF THE PROPERTY OF THE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
"~+~hes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SO
                                                                                                                                                                                                                                                                                           InterPro; IPR001909; KRAB.
InterPro; IPR000822; Znf-C2H2.
InterPro; IPR000822; Znf-C2H2.
Pfam; PF00152; KRAB; 1.
Pfam; PF00096; Zf-C2H2; 10.
PRINTS; PR00048; ZINCFINGER.
SMART; SM00349; KRAB; 1.
SMART; SM00355; ZnF_C2H2; 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2257_HUMAN
Q9Y2Q1;
16-OCT-2001
16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
CONFLICT
SEQUENCE
DOMAIN
DOMAIN
ZN_FING
ZN_FING
ZN_FING
ZN_FING
ZN_FING
ZN_FING
ZN_FING
                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Han Z.-G., Zhang Q.-H., Ye M., Kan L.-X., Gu B.-W., He K.-L., Shi S.-L., Zhou J., Fu G., Mao M., Chen S.-J., Yu L., Chen Z., "Molecular cloning of six novel Kruppel-like zinc finger genes from hematopoietic cells and identification of a novel transregulatory domain KRNB.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zinc finger protein ZNF257 OR BMZF4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF070651; AAD HSSP; P08047; 1SP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Biol. Chem. 274:35741-35748(1999).
-!- FUNCTION: MAY FUNCTION AS A TRANSCRIPTION FACTOR.
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Bone marrow; MEDLINE=20054457; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: CONTAINS 1 KRAB DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168 SDGFFELESQPKR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 SDGFYTMENSDRR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FINGER PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184
419
464 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
protein 257 (Bone marrow zinc finger 4) (BMZF-4).
    173
173
201
229
229
257
288
316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD20957.1; -.
  Repeat.
75
509
195
223
223
251
282
310
338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=10585455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184
424
49999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MW;
ZINC FINGERS.
CCH2-TYPE.
CCH2-TYPE.
CCH2-TYPE.
CCH2-TYPE (DEGENERATE).
CCH2-TYPE.
CCH2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 38; DB Pred. No. 32; 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      V -> VV (IN REF. 1).
LHLVGD -> PTFSWR (IN REF. 1).
; 2BFFEFD363A3F173 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
```

```
밁
             δÃ
                                                               SOSTE
                           Query Match
Best Local S
Matches 7
                                                              ZN_FING
ZN_FING
ZN_FING
ZN_FING
ZN_FING
ZN_FING
ZN_FING
154 FYKFSNSDRHK 164
              5 FYTMENSDRRK 15
                          Similarity 7; Conserv
                                                               535
                                                                      344
372
403
431
459
487
                           Conservative
                                                               Ã,
                                                             366
397
425
453
481
509
62348 MW;
                                   47.5%;
63.6%;
                            0
                           Score 38; DB Pred. No. 37; O; Mismatches
                                                                     C2H2-TYPE
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
                                                                                                        C2H2-TYPE
                                                               .22DC5B0C4613BC51 CRC64;
                                  DB 1;
37;
                                                                                                 (ATYPICAL).
                                         Length 535;
                            Indels
                           0,
                          Gaps
```

Search completed: June 10, 2002, 15:29:43 Job time: 478 sec

```
PRESULT

ON THE PROPERTY OF TH
     RESULT
Q980A6
                                                                                                       밁
                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9LIM5;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GENOMIC DNA, CHROMOSOME 3, BAC CLONE: 44B12.
Arabidopsis thaliana (Mouse-ear Cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core everosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-21297186; PubMed-11404009; Lee L.T.O., Nong G., Chan Y.H., Tse D.L.Y., Cheng C.H.K. "Molecular cloning of a teleost growth hormone receptor functional interaction with human growth hormone."; Gene 270:121-129(2001).
EMBL; AF293417; AAK60495.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GHR.
                                                                                                                                                                                                                                                                                                                                                                                                    "Structural analysis of A Sequence features of the TAC and BAC clones.";
DNA Res. 7:217-221(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN-COLUMBIA; Kaneko T., Kato T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carassius auratus (Goldfish).
Eukaryota, Metazoa; Chordata; Craniata;
Actinopterygii, Neopterygii; Teleostei;
Cypriniformes; Cyprinidae; Carassius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, GROWTH HORMONE RECEPTOR.
                                                                                                                                                                                                                                                                                                                            EMBL; AP001299; BAB02564.1;
EMBL; AP000370; BAB02564.1;
SEQUENCE 684 AA; 75577 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nakamura Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20363099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=7957;
                                                                                                    329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  щ.
                                                                                                                                                  1 MSDGFYTMENSDRRK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MSDGFYTMENSDRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VSDGAYTSENTARQ
                                                                                                    LNDGVYTEEEEDERR
                                                                                                                                                                                                   Similarity 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 57.8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MAR-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       602 AA;
                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=10907853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sato
) to t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67262 MW;
                                                                                                                                                                                                                        52.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52.5%;
                                                                                                    343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana chromosome regions of 4,251,695 bp covered
                                                                                                                                                                                                                                                                                                                            MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last
Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , Nakamura Y., Asamizu E., Ta
EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                              Score 42; DB
Pred. No. 49;
3; Mismatches
                                                                                                                                                                                                   ω
``
                                                                                                                                                                                                                                                                                                                                                      JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 42; DB
Pred. No. 43;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4D9F66821C1A029E CRC64;
                                                                                                                                                                                                                                                                                                                            6A4714690761B66A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence update)
annotation update)
                                                                                                                                                                                                                          DB
49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vertebrata; Euteleostomi;
Euteleostei; Ostariophysi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                   ა
,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   bp covered by ninety P1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ω
••
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 602;
                                                                                                                                                                                                                                            Length 684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.H.K.;
                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a; Tracheophyta;
eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ostariophysi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tabata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and
                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
Q45606
В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A CONTRACTOR OF THE CONTRACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q980A6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archaea;
                                                                                                                                                                                                                                                                                             DNA Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RPS6E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G
```

```
Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C STRAIN-ATCC 35092 / DSM 1617 / P2;

X MEDLINE=21332295; PubMed=11427776;

A She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

A Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

A Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Pen

A Thi Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup

Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

A Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

"The complete genome of the crenarchaeon Sulfolobus solfataric

Proc., Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).

R EMBL; AE006674; AAK40739.1; ".

EMBL; AE006674; AAK40739.1; ".

BENDINGS, Ebborgan L. Se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q45606;
Q45606;
Q1-NOV-1996
Q1-NOV-1996
                                                                        Zhang J., Aronson A.I.;
Zhang J., Aronson A.I.;
"A Bacillus subtills bglA gene encoding phospho-beta-glucosidase inducible and closely linked to a NADH dehydrogenase-encoding gene 140:85-90(1994).
                                                                                                                                                                                                                                                      Ogasawara N., Nakai S., Yoshikawa H.; "Systematic sequencing of the 180 kilobase region of the Bacillus subtilis chromosome containing the replication origin.";
                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Bacillus/Staphylococcus
CBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01092; Ribosomal_S6e; 1.
ProDom; PD003460; Ribosomal_S6E; 1.
Ribosomal protein; Complete proteome.
SEQUENCE 214 AA; 23720 MW; 9E20B93EB0247693 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2001 (TrembLrel.
01-OCT-2001 (TrembLrel.
01-OCT-2001 (TrembLrel.
SSU RIBOSOMAL PROTEIN S6
                                                                                                                                                                                                                                                                                                                     MEDLINE-96051385; PubMed-7584024;
                                                                                                                                                                                                                                                                                                                                            STRAIN-168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sulfolobus solfataricus
MEDLINE-94156824; PubMed-8113162
                                       SEQUENCE FROM
                                                                                                                                                       MEDLINE=94171085; PubMed=8125345;
                                                                                                                                                                              STRAIN-168;
                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=2287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GFYPNENGERRR 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GFYTMENSDRRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 58.: 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UNKNOWN.
                                                                                                                                                                                                                                      chromosome co
1:1-14(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     enarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 18, C
18, I
1 18,
N S6E (
                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus/Clostridium group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          00,
10,
10,
                                                                                                                                                                                                                                                                                                                                                                                                                      group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sulfolobales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (RPS6E).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence up
Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41; DB
Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sulfolobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ω
--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           solfataricus.P2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 na N., Peng
Tolstrup N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sulfolobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Α.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           `.=
```

```
REPUBLICAN CONTRACTOR 
                                                                                                                                                                                                                           RA Borniss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., RA Brouillet S. Brunschi C.V., Caldwell B., Capuano V., Carter N.M., RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., RA Choi S.K., D., Errington J., Fabret C., Ferrari E., Foulger D., RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., Ra Gilseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A., RA Gliseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A., RA Hilbert H., Holsappel S., Koningstein G., Krogh S., Kumano M., Vones L., Kasahara Y., Klaerr Blanchard M., Klein C., Ra Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C., Ra Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C., Ra Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., RA Persecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Ra Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., RA Persecan E., Polla C., Rocha E., Roche B., Rose M., Sadaie Y., RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B., Ra Sekiguchi J., Takashashi H., Takemaru K., Tanakoshi A., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A., Varimork P., Varimork K., Varimork K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96093926; PubMed=7584049; Yoshida K., Seki S., Fujimura M., Miwa Y., "Cioning and sequencing of a 36-kb region of genome between the gnt and iol operons."; DNA Res. 2:61-69(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hartford O.M., Dowds B.C.;
"Isolation and characterization
mutant of Bacillus subtilis.";
Microbiology 140:297-304(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gardan R., Rapoport G., Debarbouille M.; "Expression of the rocDEF operon involve Bacillus subtilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96093926; Pul
Yoshida K., Seki S.,
STRAIN=168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Azevedo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kunst F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98044033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-168;
Kasahara Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95311309; PubMed=7540694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94236234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       activators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus subtilis, belongs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Calogero S.,
Debarbouille
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteriol. 176:1234-1241(1994).
                                                                                                                                                   complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , v.,
                                                                                                                                                                                    P., Wipat A.,
K., Yoshikawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biol. 249:843-856(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ogasawara N., Moszer I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y., Nakai S., (NOV-1995) to
                                                                                                                                                                                       Yoshikawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 regulatory protein
lis, belongs to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed-9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=8180695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R.,
                                                                                                                                                   sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ., Yoshikawa H., Ogasawara N.;
to the EMBL/GenBank/DDBJ databases.
                                                                                                                                             Yamamoto H., Yamane K., Yasumoto K., Yata K.,
H.F., Zumstein E., Yoshikawa H., Danchin A.;
sequence of the gram-positive bacterium Bacill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glaser P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          controlling arginine utilization in NtrC/NifA family of transcriptional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ۵
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Albertini A.M., Alloni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schweizer J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hydrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Fujita
of the E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in arginine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peroxide resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rapoport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ĸ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           catabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ດ
:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'n
```

```
RESULT
Q9UPS6
 밁
                                                                                                                                                                                           Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SQ RA RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       망
                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                              01-MAY-2000
01-MAY-2000
01-DEC-2001
                                                                                                                                                                                                                                                           EMBL; AF2
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D78
EMBL; Z99
Complete
SEQUENCE
                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001
01-DEC-2001
MEDLINE-99397452;
Kikuno R., Nagase
                  TISSUE-BRAIN;
                          SEQUENCE FROM N.A.
                                                                    Homo sapiens (Human).
                                                                              KIAA1076
                                                                                      KIAA1076 PROTEIN
                                                                                                                                  Q9UPS6
                                                                                                                                                                                                                                                                             Submitted
                                                                                                                                                                                                                                                                                     Darai G.,
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                 Shrew)
                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21211637; PubMed=11312357
Bahr U., Darai G.;
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                      Betaherpesvirinae.
                                                                                                                                                                                                                                                                                                                                                                                                              Tupaia herpesvirus.
Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q91TS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted
                                                                                                                                                                                                                                                                                                                        "Analysis and Characterization Shrew) Herpesvirus.";
J. Virol. 75:4854-4870(2001).
                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131
                                                                                                                                                                            594 MPHGEYTIEDEDRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 SDGFYTMENS
                                                                                                                                                                                              MSDGFYTMENSDRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TDGFYTLYNS
                                                                                                                                                                                                                                                          tted (JUN-2000) to the EMBL/GenBank/DDBJ databases AF281817; AAK57065.1; -. NCE 636 AA; 72058 MW; F6489A4BAD99FE85 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F., Ogasawara N., Yosh
tted (NOV-1997) to the
D78193; BAA11286.1; -.
Z99124; CAB16064.1; -.
                                                                                                                                                                                                              Similarity
8; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      387 AA;
                                                                                                                                                                                                                                                                                     Bahr U.;
                                                                                             (TrEMBLrel.) (TrEMBLrel.) (TrEMBLrel.)
                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11
                                                                                       (FRAGMENT)
PubMed=10470851;
T., Ishikawa K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44247 MW;
                                                     Primates;
                                                                                                                                                                            607
                                                                                                                                                                                             14
                                                            Chordata;
                                                                                                                                                                                                                        51.2%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51
70
                                                                                               13,
13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                          19,
19,
                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yoshikawa H.,
                                                                                                                                                                                                                                                                                                                                                                                                               RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation updat
                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL/GenBank/DDBJ databases.
                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2
                                                                                                                                                                                                             Pred. No. 69;
2; Mismatches
                                                                                                                                                                                                                        Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
Pred.
                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                          of the Complete Genome of Tupaia (Tree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5EC34B07BA975BB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No.
Hirosawa
                                                                                                                                  804 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Danchin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
                                                                                                                                                                                                                                 12;
:
:
                                                                                                                                                                                                                                                                                                                                                                                                                                         update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Α.;
                                                                                                                                                                                                                4;
                                                                                                                                                                                                                                Length 636
Miyajima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 387
                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
```

```
PRESULTATION OF THE PRESUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
""" hes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . છુ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RAT DR RT DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
Trembirel. 01, C

vi-DEC-2001 (Trembirel. 19, La.

DE TB-292 MEMBRANE ASSOCIATED PROT

Trypanosoma brucei.

Trypanosoma brucei.

Eukaryota: Euglenozoa; Kinetopl-

Eukaryota: Euglenozoa; (1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O943J4 PRELIMINARY;
O943J4;
O1-DEC-2001 (TremBLrel. 19, C
O1-DEC-2001 (TremBLrel. 19, I
O1-DEC-2001 (TremBLrel. 19, I
PUTATIVE S-RECEPTOR KINASE.
P0039A07.12.
                                                                                                                                                                                                                                                                          Q26775
Q26775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Receptor; SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yaman
"Oryza sativa nipponbare(GA3)
clone:P0039A07.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (Rice).
Eukaryota; Viridiplantae; Stre
Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza
MCBI_TaxID=4530;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (FEB-2001) to the EMBL; AP003235; BAB64106.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00508; POSTSET; 1.
SMART; SM00317; SET; 1.
PROSITE; PS50280; SET; 1.
NON_TER 1 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00856; SET;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003616; PostSET.
InterPro; IPR001214; SET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TDGFYTMAN 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDGFYTMEN 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDGFYTMENSDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEGFYTIDKKDK 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            804 AA; 87997 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90696 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51.2%;
77.8%;
                                                                                        Kinetoplastida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yamamoto K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptophyta;
                                                                                                                                                        PROTEIN.
                                                                                                                                                                                 Created)
Last sequences
Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 41; DB
Pred. No. 89;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ۲;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liliopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96C0E1FDACE42F27 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13CAB0BA5420BE67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                 sequence update) annotation updat
                                                                                                                                                                                                                                                                                                         2550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unidentified human clones from brain w
                                                                                        Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Embryophyta; Tracheophyta; ; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                         B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromosome 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4
                                                                                                                                                                                 update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         n genes. XIV which code
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
```

```
RESULT
054026
                                                                                                                                                                                                           RESULT
Q9RZJ9
                                                                                                                                                                                                                                                    Вb
                                                                                                                                                                                                                                                                                                                                                ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RAT RATE
                                                                                                                                                                                                                                                                       24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ş
                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 7
                 MEDLINE=20036896; PubMed=10567266; White O., Elsen J.A., Heldelberg J. Dodson R.J., Haft D.H., Gwinn M.L., Moffat K.S., Qin H., Jiang L., Pampl
                                                                                                                                          01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
HEMOLYSIN, PUTATIVE.
                                                                                                                                                                                                                                                                                                                                                        Reijnders W.N.M., Harms N.;
Paracoccus denitrificans, MxaA, MxaC, MxaK, Nsubmitted (JAN-1998) to the EMBL/GenBank/DDBJ EMBL; AJ000884; CAA04384.1;
CHAIN 2 144 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1998 (TrEMBLrel. 01-DEC-2001 (TrEMBLrel. 01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          054026
054026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lee M., Russell D., D'Alesandro P., Van der Ploeg L
"Identification of membrane associated proteins in
encoding an internal, EARLRAEE amino acid repeat.";
J. Biol. Chem. 269:8408-8415(1994).
EMBL; X73956; CAA52142.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-427-60;
MEDLINE-94179225; PubMed-8132566;
                                                            STRAIN-R1;
                                                                                                             Deinococcus radiodurans.
Plasmid MP1.
                                                                                                                                                                                      Q9RZJ9;
                                                                                                                                                                                                 Q9RZJ9
                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                      SEQUENCE FROM N.A.
                                                                                                                                   DRB0128
                                                                                        Bacteria; Thermus/Deinococcus
NCBI_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-PD1222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Paracoccus denitrificans
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Paracoccus
                                                                                                                                                                                                                                                    66 TDGYYSDDNEDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10
                                                                                                                                                                                                                                                               2 SDGFYTMENSDR
:||:|: :| ||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSDGFYTMENSDRRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MADGCYAVSREDRQK 2251
                                                                                                                                                                                                                                                                                            Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 46.7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                144 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2550 AA;
                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                     77
                                                                                                                                                                                                                                                                                                                                                16695 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51.2%;
46.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    289354 MW;
                                                                                                                                                                                                                                                                                                        50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06,
19,
                                                                                                                                                      13,
13,
                                                                                                                                                                                                                                                                                                       .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alpha subdivision; Rhodobacter group;
                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                            Score 40; DB
Pred. No. 20;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 41; DB Pred. No. 3.1e 3; Mismatches
                                                                                                   group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
M.L., Nelson W.C., na.
M.L., Nelson W.C., na.
Crosby M., S
                  Pamphile
                                                                                                                                                                                                                                                                                                                                                849D32E80773C780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    484C297B65A8D376 CRC64;
                                                                                                   Deinococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 5;
3.1e+02;
3.3 5;
                                                                                                                                                                                                                                                                                                     DВ
20;
                                                                                                                                                                                                                                                                                                                                                                              MxaK, MxaL, MxaD and orf's.";
nk/DDBJ databases.
                                                                                                                                                                                                AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2550;
                                                                                                                                                                                                                                                                                                                 Length 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trypanosoma
                                                                                                   Deinococcus
                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
```

```
RESCUT
Q97P13
ID 7P13
ID 7P13
AC Q99
DT 011
CC St COC ST C
Q9HQP0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Thes 7; Conserve
                                                                                                                        Ъ
                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D., Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D., Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L., McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey i Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.; "Complete genome sequence of a virulent isolate of Streptococcus pneumoniae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q97P13;
01-OCT-2001
01-OCT-2001
01-DEC-2001
Q9HQP0
                                                                                                                                                                                                                                                                                                                                      Science 293:498-506(2001).
EMBL; AE007475; AAK75904.1;
TIGR; SP1831; -
Hypothetical protein; Complete
SEQUENCE 160 AA; 18699 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2001 (Tremblrel 18, 01-OCT-2001 (Tremblrel 18, 01-DEC-2001 (Tremblrel 19, 14, PROTEIN SP1831.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q97P13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.";
Science 286:1571-1577(1999).
SCIENCE, AE001826; AAF12559.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SP1831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01595; DUF21; 1. SMART; SM00116; CBS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21357209; PubMed=11463916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002550; DI
Pfam; PF00571; CBS; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGR; DRB0128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vamathevan J.J.,
Makarova K.S., A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000644; CBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fraser C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ketchum K.A., Nelson
                                                                                                                      114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          347 SDGFWIQENGD
                                                                                                                                                                 1 MSDGFYTMENSDRRK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 SDGFYTMENSD
                                                                                                                      MSDGFYEFYQNNQNK
                                                                                                                                                                                                                       Similarity 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome.
437 AA; 47593 MW;
PRELIMINARY;
                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ., Lam P., McDonald L., Utterback T., Zalewski C., Aravind L., Daly M.J., Minton K.W., Fleischmann F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12
                                                                                                                                                                                                                                         48.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ad L., Daly M.J., Minton K.W., Fleischmann K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DUF21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ۲.
                                                                                                                                                                                                                                         Score 39; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40;
Pred. No.
                                                                                                                                                                                                             Pred. No. 34;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                 proteome.
6ECA8F048E9E4C11 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1626ABD7440C50A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160
                                                                                                                                                                                                                                                                 DΒ
                                                                                                                                                                                                                                                                 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                group; Streptococcaceae;
                                                                                                                                                                                                                'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ω,
                                                                                                                                                                                                                                                           Length 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 437
                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                円.K.,
                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
```

```
RESULT
Q9VW84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Thehes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 16, Last sequence update)
GLYCEROL-3-PHOSPHATE DEHYDROGENASE CHAIN A.
GPDAI OR VNC1070G.
Halobacterium --
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Bortis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Cherry J.M., Cawley S., Dahlke C., Mays A.D., Dew I., Dletz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn I Durbin K.J., Evangelista C.C., Ferriera S., Fleischmann 1 Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
                                                                                                                                                                                                                                     Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Aphayani A., An H.-J., Andrews-Pfannkoch C., Baddwin D., Ballow B.W., Basin, Backley B. B. Barter B.D., Ballow B.W., Basin, B.W., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
"Genome sequence of Halobacterium species NRC-1.";
Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
EMBL; AE005039; AAG19473.1;
InterPro; IPR000447; FAD_Gly3P_dh.
PRINTS; PR01001; FADG3PDH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9VW84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9HQP0;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CG7328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9VW84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome. SEQUENCE 187 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE-20504483; PubMed-11016950;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=64091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Halobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaea; Euryarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSDGFYTMENSDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISRGFYVLDHADR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19735 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13,
13,
17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Halobacteriales; Halobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        933A226B16789311 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           306 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                        Chandra I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
              Σ.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
```

```
8
                                                                                                                              Query Match
Best Local Similarity
Watches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Laik M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Syier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Yelliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Yelliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Yelliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Gibbs R.A., Myers E. W., Zhong W., Zhon W., Zhong G., Zhong L.,
RT The genome sequence of Drosophila melanogaster.";
RI Science 287:2185-2195(2000)
DR Parker D. Corroll S., Parker S., 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-MALISH 7;
MEDLINE-21442074; PubMed-11557893;
Ogata H., Audic S., Renesto-Audiffren P., Fo
Samson D., Roux V., Cossart P., Weissenbach
Raoult D.;
                                                                                                                                                                                                                                                                                                                                                              Rickettsia conorii.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales; Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q92JN5
Q92JN5; PRELIMINARY;
Q92JN5;
Q1-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                           Complete proteome. SEQUENCE 360 AA;
                                                                                                                                                             "Mechanisms of evolution in Rickettsia conorii and R. prowazekii."; Science 293:2093-2098(2001).
EMBL; AE008571; AAL02570.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00584; PFKB_KINASES_2; 1.
SEQUENCE 306 AA; 34118 MW; 992EB9E0E9B107B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=781;
                                                                                                                                                                                                                                                                                                                                                                                                                           ECF OR RC0032.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21
   w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 DGFYTMENSDRR 14
 DGFYTMENSDRRK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NGSYPMEDTDRR 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity
7; Conserv
                                                                                                                           360 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                     Conservative
                                                                                                                             41527 MW;
                                                      48.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.8%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ω
--
                                                     Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 39;
Pred. No.
                                                                                                                           96082C390287B9C6 CRC64;
                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
70;
                                                                      DB 16; Length 360;
                                                                                                                                                                                                                                     Fournier P.-E., Barbe
ch J., Claverie J.-M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5;
                                    ω
••
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 306
                                     Indels
                                                                                                                                                                                                                                                          Barbe V.,
                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                    0
```

В

125 EGIFTSGSSDRRK 137

Search completed: June 10, 2002, 15:29:19 Job time: 489 sec

O X O X O O O O O O O O O O O O O O O O	×
06-SEP-2000. 25-FEB-1999 05-MAR-1999 05-MAR-1999 29-MAR-1999 21-APR-1999 16-APR-1999 25-MAR-1999 25-MAR-1999 26-APR-1999 27-APR-1999 28-APR-1999 28-APR-1999 28-APR-1999 28-APR-1999 28-APR-1999 29-APR-1999 21-APR-1999 21-APR-1999 21-APR-1999 22-APR-1999 23-APR-1999 23-APR-1999 24-MAY-1999 25-MAY-1999 26-MAY-1999 27-MAY-1999 28-MAY-1999 28-MAY-1999 29-MAY-1999 21-JUN-1999 21-JUN-1999 21-JUN-1999 22-JUN-1999 23-JUN-1999 24-JUN-1999 25-MAY-1999 26-MAY-1999 27-JUN-1999 28-JUN-1999 28-JUN-1999 29-JUN-1999 29-JUN-1999 29-JUN-1999 21-JUN-1999 21-JUN-1999 21-JUN-1999 21-JUN-1999 21-JUN-1999 22-JUN-1999 23-JUN-1999	
2000EP-0301439. 99US-0121825. 99US-0123180. 99US-0123548. 99US-012578. 99US-0126785. 99US-0126785. 99US-0126785. 99US-0126786. 99US-0130449. 99US-0132484. 99US-0132484. 99US-0132486. 99US-0132486. 99US-0134218. 99US-0134241. 99US-0134241. 99US-0139425. 99US-0139456. 99US-0139456. 99US-0139458. 99US-0139459. 99US-0139459. 99US-0139459. 99US-0139459. 99US-0140893. 99US-0140893. 99US-0141842. 99US-0141842.	
"" " " " " " " " " " " " " " " " " " "	-
06-701-1999 08-701-1999 11-701-1999 11-701-1999 11-701-1999 11-701-1999 11-701-1999 11-701-1999 11-701-1999 11-701-1999 11-701-1999 11-701-1999 11-701-1999 11-701-1999 11-701-1999 12-701-1999 12-701-1999 12-701-1999 12-701-1999 12-701-1999 12-701-1999 12-701-1999 12-701-1999 12-701-1999 12-701-1999 12-701-1999 12-701-1999 12-701-1999 12-701-1999 12-701-1999 12-701-1999 12-701-1999 13-701	JUL-199
990S-0142900 990S-0142900 990S-0142970 990S-0144005 990S-0144306 990S-0144352 990S-0144331 990S-0144331 990S-0144332 990S-0144331 990S-0144331 990S-0145086 990S-0145088 990S-0145088 990S-0145088 990S-0145088 990S-0145088 990S-0145088 990S-014508 990S-014508 990S-014508 990S-0145218 990S-0145218 990S-0145218 990S-0146388 990S-0147403 990S-0147403 990S-0149723 990S-0159788	9US-0142

```
AAGO6339
ID AAGO
XX
AC AAGO
XX
DT 17-C
XX
DE Arak
XX
Prot
KW Prot
KW hybi
KW term
XX
COS Arak
XX
PR
PR
PR
25-1
PR
05-1
                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                    δÃ
                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                        22-SEP-1999
23-SEP-1999
24-SEP-1999
28-SEP-1999
28-SEP-1999
24-OCT-1999
05-OCT-1999
05-OCT-1999
07-OCT-1999
13-OCT-1999
13-OCT-1999
14-OCT-1999
14-OCT-1999
14-OCT-1999
14-OCT-1999
14-OCT-1999
14-OCT-1999
12-OCT-1999
21-OCT-1999
22-OCT-1999
23-OCT-1999
25-OCT-1999
26-OCT-1999
26-OCT-1999
27-OCT-1999
28-OCT-1999
28-OCT-1999
28-OCT-1999
28-OCT-1999
    25-FEB-1999;
05-MAR-1999;
                             25-FEB-2000;
                                              06-SEP-2000
                                                                EP1033405-A2
                                                                                Arabidopsis thaliana.
                                                                                                 Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                    Arabidopsis
                                                                                                                                                                       AAG06339
                                                                                                                                                                                        AAG06339 standard;
                                                                                                                                                      17-OCT-2000
                                                                                                                                                                                                          11
                                                                                                                                                                                                                                    H
                                                                                                                                                                                                                                                     ļ
                                                                                                                                                                                                                                  1 MSDGFYTMENSD 12
||||:|: : :|
| msdgyysskktd 12
                                                                                                                                                                                                                                                                     h 48.8%;
Similarity 50.0%;
6; Conservative
                                                                                                                                   thaliana protein fragment SEQ ID
                             2000EP-0301439
                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                      9908-015519

9908-0156496

9908-0156496

9908-0156599

9908-0157753

9908-0158202

9908-0158202

9908-0158202

9908-0159294

9908-0159294

9908-0159294

9908-0159330

9908-0159331

9908-0159538

9908-0159584

9908-0160767

9908-0160767

9908-0160768

9908-0160767

9908-0160814

9908-0161404

9908-0161404

9908-0161361

9908-0161361

9908-0161361

9908-0161361

9908-0161361

9908-0161361

9908-0161361

9908-0161361

9908-0161361

9908-0161361

9908-0161361

9908-0161361
   99US-0121825
99US-0123180
                                                                                                                                                                                       Protein; 424
                                                                                                                                                                                                                                                                    ; Score 39; DB
; Pred. No. 1.4e
4; Mismatches
                                                                                                                                                                                       A
                                                                                                                                                                                                                                                                  DB 21; Le
. 1.4e+02;
. has 2;
                                                                                                                                   NO: 3078
                                                                                                                                                                                                                                                                                      Length 387;
                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                     0;
   23 JUN 1999
23 JUN 1999
24 JUN 1999
28 JUN 1999
29 JUN 1999
30 JUN 1999
01 JUL 1999
01 JUL 1999
02 JUL 1999
06 JUL 1999
08 JUL 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
06-APR-1999;
08-APR-1999;
16-APR-1999;
                                                                                                                                 18-JUN-1999
18-JUN-1999
18-JUN-1999
18-JUN-1999
18-JUN-1999
18-JUN-1999
18-JUN-1999
18-JUN-1999
21-JUN-1999
21-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-APR-1999;
04-MAY-1999;
05-MAY-1999;
06-MAY-1999;
 12-JUL-1999;
13-JUL-1999;
14-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                          24-MAY-1999;
25-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                    14-MAY-1999;
18-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                     14-MAY-1999;
14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-APR-1999
23-APR-1999
                                                                                                                                                                                                                                                                                                                                                         28-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-APR-1999
                                                                                                                                                                                                                         18-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -APR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1999
990S-0132484

990S-0132484

990S-0132486

990S-0132486

990S-0134218

990S-0134218

990S-0134218

990S-0134221

990S-0134221

990S-0134221

990S-0135124

990S-0135124

990S-0135124

990S-013522

990S-0136021

990S-0136021

990S-0136021

990S-0137528

990S-013945

990S-014055

990S-014282

990S-014282

990S-014282

990S-014289

990S-014282

990S-014282

990S-014282

990S-014282

990S-014282

990S-014282

990S-014282

990S-014282

990S-014282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0123548.
99US-0125788.
99US-0126764.
99US-0126775.
99US-0128724.
99US-0128714.
99US-0128714.
99US-0128045.
99US-0130047.
99US-0130049.
99US-0130691.
```

99US-0144005. 99US-0144085. 99US-0144086. 99US-0144325.

```
RESULT 12
AAU34516
Дb
                                                                                                                                                                                                                                                                                                     Qy
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 6
                       21-MAR-2000;
23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                        14-OCT 1999;
21-OCT 1999;
21-OCT 1999;
21-OCT 1999;
21-OCT 1999;
21-OCT 1999;
21-OCT 1999;
22-OCT 1999;
22-OCT 1999;
22-OCT 1999;
25-OCT 1999;
25-OCT 1999;
25-OCT 1999;
26-OCT 1999;
26-OCT 1999;
26-OCT 1999;
26-OCT 1999;
27-OCT 1999;
28-OCT 1999;
28-OCT 1999;
28-OCT 1999;
28-OCT 1999;
29-OCT 1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-OCT-1999;
07-OCT-1999;
08-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-OCT-1999;
14-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-OCT-1999;
14-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-OCT-1999;
13-OCT-1999;
                                                                                            21-MAR-2001; 2001WO-US09180
                                                                                                            27-SEP-2001.
                                                                                                                              WO200170955-A2
                                                                                                                                              Escherichia coli.
                                                                                                                                                              Antisense; prokaryotic cellular antibiotic; antibacterial; drug
                                                                                                                                                                                        E. coli cellular proliferation protein #97
                                                                                                                                                                                                          14-FEB-2002
                                                                                                                                                                                                                           AAU34516;
                                                                                                                                                                                                                                            AAU34516 standard; Protein; 572
        (ELIT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-OCT-1999
                                                                                                                                                                                                                                                                                     1 MSDGFYTMENSD
||||:|: : :|
38 msdgyysskktd
                                                                                                                                                                                                                                                                                      38
       ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                       Similarity 50.0 6; Conservative
                       2000US-191078P.
2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
2001US-269308P.
                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                        990S-0160767

990S-0160776

990S-0160770

990S-0160814

990S-0160981

990S-0160981

990S-0160980

990S-0161405

990S-0161405

990S-0161359

990S-0161359

990S-0161359

990S-0161359

990S-0161359

990S-0161359

990S-0161359

990S-0161359

990S-0161359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0158369.
99US-0159293.
99US-0159294.
99US-0159295.
99US-0159329.
99US-0159331.
99US-0159331.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0159638.
99US-0159584.
99US-0160741.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0157865.
99US-0158029.
99US-0158232.
                                                                                                                                                                                                                                                                                                    12
                                                                                                                                                                                                                                                                                                                               50
                                                                                                                                                                                                                                                                                                                              . 08;
                                                                                                                                                                                                                                                                                                                     Score 39; DB 21;
pred. No. 1.5e+02;
4; Mismatches 2
                                                                                                                                                               proliferation design.
                                                                                                                                                                                                                                            AA.
                                                                                                                                                                        protein;
                                                                                                                                                                                                                                                                                                                                       Length 424;
                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                      Gaps
```

0

0-AUG

99US-0144325
99US-0144333
99US-0144334
99US-0144334
99US-0144334
99US-01448484
99US-0145086
99US-0145086
99US-0145086
99US-0145089
99US-0145089
99US-0145218
99US-0146386
99US-0146386
99US-0147038
99US-0147038
99US-0149175
99US-0149175
99US-0149175
99US-0149368
99US-0149368
99US-0151066
99US-0151066
99US-0151066
99US-0151066
99US-0151066
99US-0151066
99US-0151303
99US-0151303
99US-0151303
99US-0151303
99US-0154018
99US-0155468
99US-0156458
99US-0156458

02-AUG-1999 03-AUG-1999

26-AUG-1999 27-AUG-1999 27-AUG-1999 27-AUG-1999 31-AUG-1999 31-AUG-1999 01-SEP-1999 01-SEP-1999 10-SEP-1999 10-SEP-1999 12-SEP-1999 22-SEP-1999 22-SEP-1999 23-SEP-1999 24-SEP-1999 24-SEP-1999 24-SEP-1999 28-SEP-1999 29-SEP-1999 29-SEP-1999

```
AAU38403
     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 7
                                   21-MAR-2000;
23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic forms that the compounts of the process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are
                                                                                                                                                                                                                                                                 WO200170955-A2
                                                                                                                                                                                                                                                                                                       Salmonella typhi
                                                                                                                                                                                                                                                                                                                                             Antisense; prokaryotic cellular proliferation protein antibiotic; antibacterial; drug design
                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                            14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU38403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU38403 standard; Protein; 572 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is the continuation of the conti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Seq ID No 10109; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haselbeck R,
Yamamoto RT,
 (ELIT-)
                                                                                                                                                                                          21-MAR-2001;
                                                                                                                                                                                                                                27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   257 ssgfhtmmnad 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 SDGFYTMENSD 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001-611495/70
ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                    typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            572 AA;
                                   2000US-191078P.
2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
2001US-269308P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                          2001WO-US09180
                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        comprise sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ohlsen
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                    cellular proliferation protein #294.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ζĽ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zyskind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 39; DB
Pred. No. 2.1e
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ر
د
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.1e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ပ်
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG00233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
                                                                                                                                                                                                                                                                                                                             gene
N-PSDB; AAC00239
                   WPI; 2000-500381/45
                                                       Dumas Milne Edwards
                                                                                                                                                                                                            06-SEP-2000.
                                                                                                                                                                      21-FEB-2000; 2000EP-0200610
                                                                                             (GEST ) GENSET
```

```
cc genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are cc Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The cc invention is also useful for the identification of potential new targets compended to identify proteins used in proliferation, to express these proteins. The antisense nucleic acids can also be used to identify proteins used in proliferation, to expressed proteins. The proteins can be used to screen compounds in rational drug discovery components. The antisense nucleic acid sequence is also useful to screen compounds in rational drug discovery components. The antisense nucleic acid sequence is also useful to screen compounds in rational drug discovery components used to screen compounds in rational drug discovery components of the proteins can be used to screen compounds in rational drug discovery components used in calcia sequence is also useful to screen compounds in rational drug discovery components used in properties and the properties and the properties are required for cell proliferation in can wide variety of organisms. The present sequence represents an component component component component component in the properties of the printed specification, but was obtained in electronic format directly from wipo at cell proliferation in electronic format directly from wipo at cell proliferation in electronic format directly from wipo at the sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haselbeck R,
Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prokaryotic cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to antisense inhibitors of genes essential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-611495/70
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAS56262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seg ID No 13996; 511pp; English.
    572 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ohlsen
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ζ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proliferation, their use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zyskind JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      identifying the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              · 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ç
```

```
Query Match
Best Local S
Matches 7
257 ssgfhtmmnad
                   2 SDGFYTMENSD 12
                                       Similarity 63. 7; Conservative
267
                                                48.8%;
                                      Score 39; DB 22; Pred. No. 2.1e+02; Vienatches 2;
                                                           Length 572;
                                        Indels
                                        0
                                        Gaps
                                        0
```

```
Human secreted
EP1033401-A2
                                                                       Human;
                                                                                                                                  06-OCT-2000
                                                                                                                                                                AAG00233;
                                                                                                                                                                                             AAG00233 standard; Protein; 100
                          Homo sapiens
                                                      therapy;
                                                      5' EST; expressed sequence tag; secreted protein; cDNA isolation;
herapy; chromosome mapping.
                                                                                                                                (first entry)
                                                                                                    protein,
                                                                                                    SEQ
                                                                                                    ID NO:
                                                                                                                                                                                             8
                                                                                                      4314.
```

99US-0122487

'n

Duclert

Ą

Giordano

```
RESULT
OPERIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Sanders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Syler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.
RA Zhence 287:2185-2195(2000).
                                                                                                                                                                                     X MEDLLINE 21442074; PubMed=11557893;
X MedLISH 7;
X MedLISH 7;
X MedLISH 7;
X Medline 21442074; PubMed=11557893;
X Medline 2142074; PubMed=11557893; PubMed=11557893; PubMed=11557893; PubMed=11557893; PubMed=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q92I17
Q92I17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier F. Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P. de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.
                                                                                                                                          Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rickettsiaceae;
NCBI_TaxID=781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; alpi
Rickettsiaceae; Rickettsieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE003826; AAF58652.1; -. F1yBase; FB90033627; CG13204. InterPro; IPR004210; BESS. Pfam; PF02944; BESS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glodek
                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hostin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Durbin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rickettsia
                                                                                                                                                                                Mechanisms of evolution in Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACYLAMINO-ACID-RELEASING ENZYME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GNAEHVASAVENANRVN 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLFONLANOVONANRLN 382
                                                                                      ce 293:2093-2098(2001)
AE008621; AAL03141.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., I
K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischn
C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.
A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
8; Conserv
proteome.
676 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conorii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (TrEMBLrel. 19, of the control of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BESS;
AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62998 MW;
    76356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47.8%;
47.1%;
    WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alpha subdivision;
eae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 43; DB 5;
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A44067E859257D12 CRC64;
9F9977DD060F6246
                                                                                                                                                                                                                                                                           Weissenbach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         676
                                                                                                                                                                                                                                                                                                                      P.,
                                                                                                                                                                                conorii and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA
                                                                                                                                                                                                                                                                       Fournier P.-E. ch J., Claverie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rickettsiales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 605
CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brottier P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                ₽.
                                                                                                                                                                                                                                                                                                                      P. -E.,
                                                                                                                                                                            prowazekii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fleischmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reese M.G.,
                                                                                                                                                                                                                                                                                                                      Barbe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chandra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S.M.,
Dunn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D.L.,
                                                                                                                                                                                                                                                                                                                      <
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                K.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Η.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₽°.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
```

Query Match

47.8%;

Score 43;

gd,

16;

Length 676;

```
ID Q93NH5
ID Q0
AC Q0
DT 00
DT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DESCRIPTION OF STATE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local
Matches
                                                                                                                                                      Q93NH5;
01-DEC-2001
01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-95115562; PubMed-7815950;
Grether-Beck S., Igloi G., Pust S., Schilz E., Decker K., Brandsch R.;
"Structural analysis and molybdenum-dependent expression of the pAO1-
"Structural analysis and molybdenum-dependent expression of the pAO1-
"nocoded nicotine analysis and molybdenum-dependent expression of the pAO1-
"nocoded nicotine analysis and molybdenum-dependent expression of the pAO1-
"Structural analysis and molybdenum-dependent expression of the pAO1-
"
    Arthrobacter nicotinovorans Plasmid pA01.
Bacteria; Firmicutes; Actino
                                                                                                                                                                                                                                                                                                                 Q93NH5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brandsch R., Submitted (FEB-1995) to the EMBL/GenBan-i- CATALYTIC ACTIVITY: NICOTINE + ACCE-HYDROXXNICOTINE + REDUCED ACCEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arthrobacter nicotinovorans Plasmid pAO1. Bacteria; Firmicutes; Actin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-OCT-2001 (TrEMBLrel.
NICOTINE DEHYDROGENASE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q59129;
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000674; Aldxan_dh_C.
Pfam; PF07315; Ald_Xan_dh_C; 1.
Pfam; PF02738; Ald_Xan_dh_C2; 1.
Oxidoreductase; Molybdenum; Plasmid.
SEQUENCE 814 AA; 87665 MW; 9C5D096EC16028E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. Brandsch R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q59129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- COFACTOR: MOLYBDOPTERIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brandsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NDHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 NAEHVASAVENANRV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INDUCTION: B
SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                              æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A MEMBRANE-ASSOCIATED FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEHYDROGENASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GNAEHVASAVENANRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAEHVVSALYHPGRV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRAEHIGDDLKNANLI 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X75338; CAA53088.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 7; Conserv
Firmicutes; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (OCT-1993)
                                                                                                                                                      (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY MOLYBDATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TO THE C-TERMINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          utes; Actinobacteria; Actinobacteridae;
Micrococcineae; Micrococcaceae; Arthro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47
60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to the EMBL/GenBank/DDBJ
IY: NICOTINE + ACCEPTOR +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16
                                                                                                                                                  19,
19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LARGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01,
01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THE ENZYME
                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
GE CHAIN (EC 1.5.99.4) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       No 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERTEBRATE XANTHINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SI
                                                                                                                                                                                                                                                                                                                     816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                814
    Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J databases + H(2)0 = (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 814;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A SOLUBLE FORM AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arthrobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (NDHC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -6-(S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
```

```
RESULT
OPERATION
P71214
ID P7
AC P7
AC P7
DT 01
DT 01
DT 01
DE ES
GN ES
OS ES
OC Ba
GO Ba
GO Ba
GO NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                         P71214
P71214;
01-FEB-1997
01-FEB-1997
01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20509816; PubMed=11055941; McGhee G.C., Jones A.L.; McGhee G.C., Jones A.L.; "Complete Nucleotide Sequence of Ubiquitous Plasmid pEA29 amylovora Strain Ea88; Gene Organization and Intraspecies Appl. Environ. Microbiol. 66:4897-4907(2000). EMBL; AF264948; AAG31047.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21405725; PubMed=11514508;
Baitsch D., Sandu C., Brandsch R., Igloi G.L.;
"Gene Cluster on pAO1 of Arthrobacter nicotinovorans Involved in Degradation of the Plant Alkaloid Nicotine: Cloning, Purification, Characterization of 2,6-Dihydroxypyridine 3-Hydroxylase.";
J. Bacteriol. 183:5262-5267(2001).
BMBL; AF373840; AAK64263.1; -.
                                     Escherichia coli.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000051; SAM_bind.
Hypothetical protein; Plasmid.
SEQUENCE 171 AA; 18916 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmid pEA29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Cr
01-MAR-2001 (TrEMBLrel. 16, La
01-JUN-2001 (TrEMBLrel. 17, La
HYPOTHETICAL 18.9 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9F807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE-21405725;
                      Escherichia
                                                                                     ESPB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-EA88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Erwinia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Erwinia amylovora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9F807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Actinomycetales; Micrococcineae; NCBI_TaxID=29320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184
                                                                                                                                                                                                                                                                                                                      82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N
                                                                                                                                                                                                                                                        10
                                                                                                                                                                                                                                                                                                                                                              GNAEHVASAVENANR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAEHVVSALYHPGRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAEHVASAVENANRV
                                                                                                                                                                                                                                                                                                                      GNIKEKASAIENASQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity
9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proteobacteria;
                                                                                                                         7 (TrEMBLrel.
7 (TrEMBLrel.
8 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      816 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                               PRELIMINARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87753 MW;
                                                                                                                                                                                                                                                                                                                                                              15
                                                                                                                                                                                                                                                                                                                                                                                                                            46.7%;
53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47.8%;
60.0%;
                                                                                                                                                                                                                                                                                                                      96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16
                                                                                                                           02,
08,
                                       gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gamma subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence up
                                                                                                                           Last sequence update)
Last annotation updat
                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                          4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                            Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABBAD9E1B2380743 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FF913BEF90185355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Micrococcaceae; Arthrobacter
                                                                                                                                                                                                                                                                                                                                                                                                                         42;
No.
                                                                                                                                                                                                            312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                            DB
47;
                                                                                                                                                                                                          A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  2
                                                                                                                         update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from Erwinia
Variation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δÃ
```

В Ş В QY

```
RESULT
Q9VM45
ID Q0
AC Q0
DT Q0
DT Q0
DT Q0
CC Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
085625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-ATCC 43895;
KMEDLINE-97045129; PubMed-8890194;
MEDLINE-97045129; PubMed-8890194;
MEDLINE-9704051 C., Kresse A.U., Guzmar Temperature- and medium-dependent sec toxin-producing Escherichia coil.";
Trect, Immun. 64:4472-4479(1996).
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN—EHEC EDL933;
Kresse A.U., Ebel F., Deibe
Submitted (MAY-1997) to the
EMBL; X96953; CAA65654.1; -
EMBL; Y13068; CAA73508.1; -
SEQUENCE 312 AA; 32644 M
                                             Q9VM45
Q9VM45;
01-MAY-2000
01-MAY-2000
01-MAY-2000
CG8902 PROTE
CG8902.
      Drosophila
Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Perna N.T., Mayhew G.F., Posfai G., Elli Kaper J.B., Blattner F.R.; "Molecular evolution of a pathogenicity escherichia coli 0157:H7."; Infect. Immun. 66:3810-3817(1998). EMBL; AF071034; AAC31499.1; -. SEQUENCE 312 AA; 32631 MW; 0E67D6F8F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               085625;
01-NOV-1998
01-NOV-1998
01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESPB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98339885; PubMed=9673266;
Perna N.T., Mayhew G.F., Posfai G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN=EDL933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     085625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L0020.
                                                                                                                                                                                                                                                                                            197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                197
                                                                                                                                                                                                                           12
                                                                                                                                                                                                                                                                                                                                     ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        w
                                                                                                                                                                                                                                                                                                                     AEHVASAVENANRVNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AEHVASAVENANRVNK
                                                                                                                                                                                                                                                                                          AEDLADAAEKTSRINK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AEDLADAAEKTSRINK 212
                                                                      PROTEIN
                                                                                                                                                                                                                                                                                                                                                                              8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
      melanogaster (Fruit Metazoa; Arthropoda;
                                                                                        ) (TrEMBLrel. 13, 0) (TrEMBLrel. 13, 0) (TrEMBLrel. 13, 0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                  46.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46.7%;
                                                                                                                                                                                                                                                                                          212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Deibel C., Chakraborty 7
to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98,8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gamma
                                                                                     Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                           Score 42; DB Pred. No. 94; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   w
••
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
Pred.
                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
fly).
; Tracheata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0E67D6F8F4654BCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FBEDFE52D36BA797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Guzman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           secretion of proteins h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Elliott S.,
                                                                                                                                                                                378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              island
                                                                                                                                                                                A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
      Hexapoda;
                                                                                                                                                                                                                                                                                                                                                                                                                         2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T., Guzman
J databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                                                                                                                                                         Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Donnenberg M.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRC64
                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                enterohemorrhagic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           by Shiga
                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
```

```
В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                      Q960D9
Q960D9;
01-DEC-2001
01-DEC-2001
01-DEC-2001
01-DEC-2001
SD05495P.
CGB902
                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Heterygota; Neoptera; Endopterygota; Diptera; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang 2.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).

EMBL; ABC03616; AAF52482.1; -. ElyBase; FB900031886; CG8902.

SEQUENCE 378 AA; 43809 MW; 0A365C5D2B38B2E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Lasko P., Lei Y., Lin X., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy D.M., Moshrefi A., Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Spier E., Siden Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Tunner R., Venter E., Wang A.H., Wang X., Wang R., The County C., Managarman D. A. Weinster C. M. Weissenbach T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn
Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann
Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
T., The Research C., The Control of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hostin
Jalali
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.I.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beesson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=BERKELEY;
MEDLINE=20196006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adams M.D., Celniker S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ν
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAEHVASAVENANRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NSQHIATALEKATAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 7; Conser
                                                                                                                                                                                               (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=10731132;
ker S.E., Holt R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             254
                                                                                                                                                                                                  19,
19,
                                                                                                                                                                                            Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5;
                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 42; DB 5;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Evans C.A.,
                                                                                                                                                                                                                                                                                                             A
                                                                             Hexapoda;
                                                                                                                                                                                               update)
                                                  Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gocayne
                                                                                Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ayne J.
Galle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chandra I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Д.
Т.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ۳
:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
```

```
RESULT
Q98KR2
                                                                                   00277
                                                                                                                                                                                                                                               Ωy
GE DI DI AC
                                                                                                                                   밁
                                                                                                                                                        Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                   Matches
                                                                                                                                                                                             Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                DNA Res. 7:331-338(2000).

DNA Res. 7:331-338(2000).

EMBL; APO02997; BAB48752.1; -..

InterPro; IPRO01041; Ferzedoxin.

InterPro; IPR001467; Molybdopter

Pfam; PF00311; ferz; 1.

Pfam; PF00384; molybdopterin; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2001
01-0CT-2001
01-0CT-2001
                                                           002776;
002776;
  01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
POLY(ADP-RIBOSE) GLYCOHYDROLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C. Nunco J., Pacaled J., Paragas V., Park S., Phouanenavong S., Wa Yu C., Lewis S.E., Rubin G.M., Celniker S., Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AV052108; ARX93532.1; --

SEQUENCE 395 AA; 45690 MW; 402AAB1D41CE2915 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-2001 (TremBLrel. 18, Created)
01-0CT-2001 (TremBLrel. 18, Last sequence update)
01-0CT-2001 (TremBLrel. 18, Last annotation updat
NADH-UBIQUINONE DEHYDROGENASE CHAIN 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stapleton M., Brokstein P., Hong L., Agbayani A., Champe M., Chavez C., Dorsett V., Farfan D., Frise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                        Ubiquinone;
                                                                                                                                                                                                                                                                                                                                            "Complete genome structure of Mesorhizobium loti.";
                                                                                                                                                                                                                                                                                                                                                                      Takeuchi C., Yamada M.,
                                                                                                                                                                                                                                                                                                                                                                                             Watanabe A., Idesawa K., Ishikawa A., Kawashima K.
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M.,
                                                                                                                                                                                                                                                                                                                                                                                                                       Kaneko T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=MAFF303099;
MEDLINE=21082930; PubMed=11214968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phyllobacteriaceae;
NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhizobium loti (Mesorhizobium loti)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q98KR2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q98KR2
                                                                                                                                                                                                                                                                                                                                                                                Mochizuki Y.,
                                                                                                                                   637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    257 NSQHIATALEKATAV
                                                                                                                                                                                   Local Similarity hes 8; Conser
                                                                                               15
                                                                                                                                                        1 GNAEHVASAVENANRVNK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 NAEHVASAVENANRV
                                                                                                                                  GNAEDIAGVAKLGGRLNK 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                    Nakamura Y., Sato S.,
                                                                                                                                                                                                                                              693 AA;
                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                         Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                               .yokawu .
Nakayama S., Naka.
---da M., Tabata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "ceria; alpha subdivision; Rhizobiaceae group;
Mesorhizobium.
                                                                                                                                                                                                                                              proteome.
74544 MW;
                                                                                                                                                                                            46.78;
44.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46.7%;
                                                                                                                                                                                                                                                                                            Ferredoxin.
Molybdopterin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16
                                                                                                                                                                                                                                                                                                                                                                                 Nakazaki N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 42; DB
Pred. No. 1.2e
5; Mismatches
                                                                                                                                                                                             Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>٠</u>.
                                                                                                                                                                                                                                                                                                                                                         the nitrogen-fixing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                        PRT;
                                                                                                                                                                                                                                              6CC39A61B38A7631 CRC64;
                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     Asamizu E.,
                                                                                                                                                                                                                                                                                                                                                                               Matsumoto M
                                                                        977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          693
                                                                                                                                                                                            2.4e+02
                                                                                                                                                                                                        DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
                                                                      A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .2e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ₽
                                                                                                                                                                                                           16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>ن</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         update)
                                                                                                                                                                                                                                                                                                                                                                                                        Kato T
                                                                                                                                                                                                                                                                                                                                                                                 :
S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 395
                                                                                                                                                                                                        Length 693
                                                                                                                                                                                                                                                                                                                                                                                                        T., Sasamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carlson
                                                                                                                                                                                                                                                                                                                                                         symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                              Matsuno
                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                   Sugimoto
                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ×
                                                                                                                                                                               Gaps
                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
```

```
Search completed: June 10, 2002, 15:29:18 Job time: 488 sec
                                                                                                                                                                                                                                                                       Query Match 46.7%; Score 42; DB 6; Length 977; Best Local Similarity 43.8%; Pred. No. 3.5e+02; Matches 7; Conservative 6; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINB-97277328; PubMed-9115250;

Lin W., Ame J.C., Aboul-Ela N., Jacobson E.L., Jacobson M.K.;

"Isolation and characterization of the cDNA encoding bovine poly(ADP-ribose) glycohydrolase.";

J. Biol. Chem. 272:11895-11901(1997).

EMBL; UT8975; AAB53370.1; -

Hydrolase.

Hydrolase.

SEQUENCE 977 AA; 110837 MW; 87D2100F979DF377 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
NCBI_TaxID-9913;
                                                                                                                                                  3 AEHVASAVENANRVNK 18
:| | : ::|||:|:
269 SEDVGTGLKNANRLNR 284
                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                 0,
```

QΥ

В

```
Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                     Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                     Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           length: 0
length: 2000000000
            100.0
100.0
55.0
55.0
51.2
50.0
48.8
48.8
48.8
                                                                                                                                                                                                                                                                                              Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIDSI/gogdata/hold-geneseq/geneseqp-embl/AA1989.DAT: *
(SIDSI/gogdata/hold-geneseq/geneseqp-embl/AA1989.DAT: *
(SIDSI/gogdata/hold-geneseq/geneseqp-embl/AA1989.DAT: *
(SIDSI/gogdata/hold-geneseq/geneseqp-embl/AA1999.DAT: *
(SIDSI/gogdata/hold-geneseq/geneseqp-embl/AA1992.DAT: *
(SIDSI/gogdata/hold-geneseq/geneseqp-embl/AA1992.DAT: *
(SIDSI/gogdata/hold-geneseq/geneseqp-embl/AA1993.DAT: *
(SIDSI/gogdata/hold-geneseq/geneseqp-embl/AA1993.DAT: *
(SIDSI/gogdata/hold-geneseq/geneseqp-embl/AA1995.DAT: *
(SIDSI/gogdata/hold-geneseq/geneseqp-embl/AA1996.DAT: *
(SIDSI/gogdata/hold-geneseq/geneseqp-embl/AA1998.DAT: *
(SIDSI/gogdata/hold-geneseq/geneseqp-embl/AA1999.DAT: *
(SIDSI/gogdata/hold-geneseq/geneseqp-embl/AA1999.DAT: *
(SIDSI/gogdata/hold-geneseq/geneseqp-embl/AA1999.DAT: *
(SIDSI/gogdata/hold-geneseq/geneseqp-embl/AA1999.DAT: *
(SIDSI/gogdata/hold-geneseq/geneseqp-embl/AA1990.DAT: *
(SIDSI/gogdata/hold-geneseq/geneseqp-embl/AA2000.DAT: *
(SIDSI/gogdata/hold-geneseq/geneseqp-embl/AA2000.DAT: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     June 10, 2002, 15:21:07 ; Search time 73.49 Seconds (without alignments) 22.671 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-647-522-3
80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A_Geneseq_032802: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             747574 seqs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GenCore version 4:5 Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MSDGFYTMENSDRRK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT:*
/SIDSI/gcgdata/hold-geneseq-geneseqp-emb1/AA1981.DAT:*
/SIDSI/gcgdata/hold-geneseq-geneseqp-emb1/AA1982.DAT:*
/SIDSI/gcgdata/hold-geneseq-geneseqp-emb1/AA1983.DAT:*
/SIDSI/gcgdata/hold-geneseq-geneseqp-emb1/AA1984.DAT:*
/SIDSI/gcgdata/hold-geneseq-geneseqp-emb1/AA1985.DAT:*
/SIDSI/gcgdata/hold-geneseq-geneseqp-emb1/AA1985.DAT:*
/SIDSI/gcgdata/hold-geneseq-geneseqp-emb1/AA1985.DAT:*
/SIDSI/gcgdata/hold-geneseq-geneseqp-emb1/AA1985.DAT:*
                                                                                                                                                                                                                                                                                                   DВ
            20
22
22
22
22
22
21
21
                                                                                                                                                                                                                                                                                                   ij
                           AAY33650
AAY33651
ABG11394
ABG29264
ABG29264
ABG03827
AAR75761
AAU23768
ABU23244
ABB71549
AAB71549
                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 747574
BAV3 ORF6-encoded
Novel human enzyme
Novel human enzyme
Drosophila melanog
Arabidopsis thalia
                                                                                                                                           C. rastonii hemoly
C. rastonii hemoly
Novel human diagno
Novel human diagno
Novel human diagno
                                                                                                                                                                                                                                                                                      Description
```

36	36	36	36	36	36	36	36	36	36	36	6	6	6	6	σ.	6	6	6	36.5		5	37	37	37	37	37	37	37	38	38	38	39	39
45.0	5	5	5			IJ.	ŗ	ر د	ū	45.0	5	ū	5	ŗ	ū	Š	Ġ	<u>ب</u>	5	5	Ś	6	6	5	5	<u>o</u>	9	6	7	7.	7	80	48.8
665	660	617	617	526	526	372	330	330	242	236	1153	1148	1139	1080	1080	1001	786	424	424	136	136	1162	56.7	542	537	536	408	135	238	135	100	572	572
_	2	N	_	S,	G	N	N	\vdash	N	22	N	N	N	N	N	N	N	N	0	N	0		Ν				22	22	14	22	21	22	22
AAB58885	AAB70156	AAB55987	AAY76048	AAR46928	AAR46927	AAG80995	AAB55886	AAY75947	AAG91886	ABB52667	AAM00997	AAU00511	AAM00996	AAM00897	ABG09527	AAM00784	ABG09526	ABB51126	AAW89026	ABB51128	AAW89028	AAP60720	AAU12298	AAP82864	AAP70140	AAP70142	998	10	3254	AAG90736	023	AAU38403	AAU34516
w	encodi	n cell protein		ace	cerevisiae ace	rotease and	ell protein	Murine skin cell s	m prot	richi	bon	lus su	bone	n bone n	human	n bone m	human	Human secreted pro	eptide fra	Human secreted pro	e fraq	ce of the	Human PRO9820 poly	2	0	+	phila	polypeptic	HaNPV IE-1 gene pr	tamicum pr	ecreted pr	almonella typhi	E. coli cellular p

ALIGNMENTS

RESULT AAY33650

_		_					_				_			_	_	_						_								
XX	ŢŢ	ΡŢ	PT	PT	XX	DR	XX	PI		XX	PR	XX.	PF	XX	PD	XX	PN	XX	. os	××	KW	KW	××	DE	XX	DT	××	AC	XX	ID
	mechanism -	pesticides by use of the hemolytic activity, and study of the hemolytic	stings, pharmaceuticals with blood platelet agglutination activity.	Protein with hemolytic activity, useful for drugs treating jelly fish		WPI; 1999-580740/49.		Nagai H, Nakajima T;	(SUNR) SUNTORY LTD.		01-APR-1998; 98JP-0088569.		30-MAR-1999; 99WO-JP01607.		07-OCT-1999.		WO9950294-A1.		Carybdea rastonii.		treatment; sting; jellyfish; pharmaceutical; pesticide	Hemolytic protein; blood platelet addlutination; drug development.		C. rastonii hemolytic protein derived peptide 3		06-JAN-2000 (first entry)		AAY33650;		AAY33650 standard; peptide; 15 AA.

Claim

5;

Page 23;

32pp;

Japanese

0;

В Q

Best Local Similarity

100.0%;

0,

```
8 x 0 0 0 0 0 0 0 0 x 8
RESULT
AAY33651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel protein which has hemolytic activity, blood platelet agglutination activity and a molecular weight of about 50,000 Du (by SDS-PAGE). The protein, homologs and analogs of the invention can be used as a novel approach to developing drugs useful for the treatment of jelly fish stings, pharmaceuticals with blood platelet agglutination activity, pesticides by use of the hemolytic activity, and in the study of the hemolytic mechanism. AAY33648-T33650 represent fragments of the hemolytic protein described in the invention
                                      This invention describes a novel protein which has hemolytic activity, blood platelet agglutination activity and a molecular weight of about 50,000 Da (by SDS-PAGE). The protein, homologs and analogs of the invention can be used as a novel approach to developing drugs useful for the treatment of jelly fish stings, pharmaceuticals with blood platelet agglutination activity, pesticides by use of the hemolytic activity, and in the study of the hemolytic mechanism. This sequence represents the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C. rastonii hemolytic protein.
                                                                                                                                                         Claim
                                                                                                                                                                                                  Protein with hemolytic activity, useful for drugs treating jelly fish stings, pharmaceuticals with blood platelet agglutination activity, pesticides by use of the hemolytic activity, and study of the hemolytic
                                                                                                                                                                                                                                                                                                      Naga i
                                                                                                                                                                                                                                                                                                                                                             01-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                        30-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9950294-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carybdea rastonii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hemolytic protein;
treatment; sting;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY33651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY33651 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                               (SUNR ) SUNTORY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N
                                                                                                                                                                                                                                                            1999-580740/49.
DB; AAZ23610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MSDGFYTMENSDRRK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         msdgfytmensdrrk 15
                                                                                                                                                                                                                                                                                                      Ή,
                                                                                                                                                        4; Page 26-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 100
15; Conservative
                                                                                                                                                                                                                                                                                                    Nakajima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                                                                                                                                                             98JP-0088569
                                                                                                                                                                                                                                                                                                                                                                                        99WO-JP01607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       jellyfish; .pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   blood platelet agglutination; drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein; 450 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100
                                                                                                                                                      32pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 80;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.6e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pesticide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    development;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
```

Query Match

100.0%;

Score

; 08

В

20;

Length 450;

Query Match Best Local Similarity

88 55 . 98;

Score Pred.

44; No. DB 12; 22;

Length

246;

Sequence

450

protein

described

'n

the invention

```
RESULT
ABG11394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                        polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                                               and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printer specification, but was obtained in electronic format directly from W at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, u diagnostics, forensics, gene mapping, identification of responsible for genetic disorders or other traits and t biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-OCT-2001
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; chromosome mapping; gene mapping; gene therapy;
food supplement; medical imaging; diagnostic; genetic of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human diagnostic protein #11385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG11394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG11394 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  food supplement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  363 msdgfytmensdrrk 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MSDGFYTMENSDRRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-639362/73
DB; AAS75581.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID No 41753; 103pp; English.
246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0540217
2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          relates to isolated polynucleotide (I) and
₽Ą;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŢΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1.4e-05;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mutations
to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 forensic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                   from WIPO
                                                                                                       printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
```

밁 õ

217

Matches

```
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC cand gene mapping, and in recombinant production of (II). The CC polymucleotides are also used in diagnostics as expressed sequence tags (CC for identifying expressed genes. (I) is useful in gene therapy techniques (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as imaging of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. CC diagnostics, forensics, gene mapping, identification of mutations or responsible for genetic disorders or other traits to assess biodiversity amino acid sequences. ABG00010-ABG30377 represent novel human CC Note: The sequence data for this patent did not appear in the printed at fire wiso int/nub/nub/shed not sequences.
                       Query Match
Best Local
                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                               The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human diagnostic protein #29255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medicál imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG29264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG29264 standard; Protein; 246 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 GFYTMENSD 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gfypmensd 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID No 59623; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0540217.
2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                           ÃĂ,
                 55.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TY
             Score 44; DB
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                           Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG03827
                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAS68014.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG03827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                217 gfypmensd 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 GFYTMENSD 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-639362/73
                                                                        804 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
              51.2%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ΥŢ
```

ABG29264
XX
ABG2
XX
ABG2
XX
ABG2
XX
ABG2
DT 18-F
XX
Humg
XX
Humg
XX
Hong
XX
Ho

Best Local Similarity Matches 8; Conserv

Conservative

0;

Mismatches

22; ۲.

Length 246;

Indels

0,

Gaps

0

Conservative

Score 41; DB 22; Pred. No. 1.4e+02; Mismatches

Length 804 Indels

0

Gaps

0

```
and in recombinant production of (II). The polypucleotides are also used in diagnostics as expressed sequence tags (I): (II) is useful in gene therapy techniques (I): (II): (II) is useful for generating antibodies against it, detecting or (II): (II) is useful for generating antibodies against it, detecting or (II): (II) is useful for generating antibodies against it, detecting or (II): (II): and its binding partners are useful in medical activity. (II): and (III): and (III): are useful in medical (II): (II): are useful for treating (II): (II): are useful in medical (II): (II): are useful for treating (II): are useful for treating (II): are useful for treating (II): are useful for treati
Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromo and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; SEQ ID No 34186; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human diagnostic protein #3818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; chromosome mapping; gene mapping; gene therapy; forensic food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG03827 standard; Protein; 804 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  forensic;
```

δÃ

N

0;

```
뫄
                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BAV3; vector; vaccine; gene therapy; fiber protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR75761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR75761 standard;
                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BAV3 ORF6-encoded protein
                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
BAV3 strain WBR-1 genomic DNA, from between 77 and 92 m.u., was cloned into plasmids and sequenced. ORFs that had the potential to encode polypeptides of at least 50 amino acids
                                                            Bovine adenovirus expression vector system - comprising insertion required genes into deletions in El and E3 and transformation of mammalian cell lines, useful in vaccines and gene therapy
                                                                                                               WPI;
                                                                                                                                                                                                                                     WO9516048-A
                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                             Modified-site
                                        Disclosure; Fig.7H-R;
                                                                                                                                  Babiuk LA,
                                                                                                                                                                           09-DEC-1993;
                                                                                                                                                                                            09-DEC-1994;
                                                                                                                                                                                                                 15-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             587
                                                                                                                                                      (UYSA-) UNIV SASKATCHEWAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDGFYTMENSDR 13
{:||||:: |:
segfytidkkdk 598
                                                                                                    1995-224330/29
DB; AAQ90769.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          adenovirus type 3
                                                                                                                                  Graham FL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                          93US-0164292
                                                                                                                                                                                             94WO-CA00678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers 99..101
                                                                                                                                                                                                                                                                   /label= N-glycosylation_site
973..975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= N-glycosylation_site
257..259
                                                                                                                                                                                                                                                                                                                                                                                                                               426..428
                                                                                                                                                                                                                                                                                                                                                                                                                                                   268..270
                                                                                                                                                                                                                                                                                                                                                                                                /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                         'label = N-glycosylation_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'label= N-glycosylation_site
                                                                                                                                                                                                                                                       /label= N-glycosylation_site
                                                                                                                                                                                                                                                                                               label N-glycosylation_site
                                                                                                                                                                                                                                                                                                                                    /label=_N-glycosylation_site
                                                                                                                                                                                                                                                                                                                                                        'label N-glycosylation_site
                                                                                                                                                                                                                                                                                                                                                                                                                   'label=
                                                                                                                                                                                                                                                                                                                  'label= N-glycosylation_site
                                                                                                                                                                                                                                                                                                                                                                            label = N-glycosylation_site
                                                                                                                                                                                                                                                                                                                                                                                                                                     label N-glycosylation_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   label- N-glycosylation_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                        159pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                  N-glycosylation_site
                                                                                                                                                                                                                                                                                                                                                                                               N-glycosylation_site
                                                                                                                                   Mittal SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A
                                                                                                                                   Prevec
                                                                                  of
```

```
RESULT
AAU23768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSSSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AAR75756-61) w
N-terminus of t
identity with t
similarity in t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ligase; hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; neurological disorder; metabolic disorder; inflammatory disorder; cardiovascular disorder; reproductive disorder; blood-related disorder; infectious disorder: cytosfatio cardiovascular disorder; reproductive disorder; cytosfations disorder; cytosfatio cardiovascular disorder: cytosfatio cytos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU23768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU23768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200155301-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nephrotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human enzyme polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-JAN-2001; 2001WO-US01239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-MAY-2000;
                                                                                                                     14-AUG-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 msdglytkdn 113
                                                                                                                                                                     14-AUG-2000;
                                                                         4-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MSDGFYTMEN 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the o
2000US-0225268
2000US-0225270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0179065
                                                                         2000US-0225266
                                                                                                                                              2000US-0224519
                                                                                                                                                                     2000US-0220964
2000US-0224518
                                                                                                                                                                                                                        2000US-0218290
2000US-0220963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  anticoagulant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disorder; infectious disorder; cytostatic; anti arthritic;
                                                                                                                                                                                                                                                                        2000US-0217496
                                                                                                                                                                                                                                                                                                  2000US-0217487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e identified. The amino acid sequence at the ORF6-encoded protein shared approx. 60% HAd2 fiber protein tail, but there was little knob region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #854.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             isomerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
```

-0226681

-0228924

01-SEP-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 05-SEP-2000 06-SEP-2000 06-SEP-2000 08-SEP-2000 08-SEP-2000

2000US-0230437 2000US-0229513 2000US-0229509 2000US-0229344 2000US-0229343

08-SEP-2000; 08-SEP-2000; 08-SEP-2000;

2000US-0232080

2000US-0231244 2000US-0231413

14-SEP-2000;

2000US-0232400 2000US-0232401

14-SEP-2000

2000US-0232081. 2000US-0231968. 2000US-0232397.

2000US-0232398

```
The present invention relates to the isolation of novel human enzyme completes, and the cDNA (AAS40785-AAS41684) and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the classorders including hyperproliferative disorders (e.g. cancer), communodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. carcer), communodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. arthritis), neurological disorders (e.g. AIzheimer's disease), cometabolic disorders (e.g. phenylketconuria), inflammatory disorders (e.g. arthritis), cardiovascular disorders (e.g. atherosclerosis), cometabolic disorders (e.g. henylketconuria), inflammatory disorders (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis). The blood-related disorders (e.g. haemophilia), reproductive disorders (e.g. infertility) and infectious disorders (e.g. Influenza). The colymnic polymnic polymnic polympitides of the invention can also be used in gene therapy.

AND22915-AAUZ3814 represent the novel human enzyme polypeptides of the
Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2000

05-DEC-2000

05-DEC-2000

05-DEC-2000

06-DEC-2000

08-DEC-2000

08-DEC-2000

08-DEC-2000

08-DEC-2000

08-DEC-2000

08-DEC-2000

08-DEC-2000

08-DEC-2000

08-DEC-2000
                                                                                                invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous
                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11;
                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ( HUMA - )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-465566/50.
DB; AAS41638.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0249212.
2000US-0249213.
2000US-0249214.
2000US-0249215.
2000US-0249216.
2000US-0249214.
2000US-0249244.
2000US-0249245.
2000US-0249264.
2000US-0249265.
2000US-0249265.
2000US-0249265.
2000US-0249265.
2000US-0249265.
2000US-0249297.
2000US-0249300.
2000US-0249300.
2000US-0250366.
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0251869.
2000US-0251989.
2000US-0251990.
2000US-0254097.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0251856
2000US-0251868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0256719
2000US-0251479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0251030
2000US-0251988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0249208
2000US-0249209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0249207
                                                                                                                                                                                                                                                                                                                                                                                                                  Ð
                                                                            A
                                                                                                                                                                                                                                                                                                                                                                                                                  No 1764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SC,
              48.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                             1180pp;
Score 39; DB Pred. No. 38; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MS
                                                                                                                                                                                                                                                                                                                                                                                                                English.
                               22;
 2
                            Length 119;
   Indels
 0
 Gaps
```

27-SEP-2000; 29-SEP-2000; 29-SEP-2000;

2000US-0235834. 2000US-0235836. 2000US-0236327.

2000US-0235484 2000US-0234998 2000US-0234997

2000US

-0236367

14-SEP-2000; 21-SEP-2000; 21-SEP-2000;

14-SEP-2000; 14-SEP-2000; 14-SEP-2000;

2000US-0233065

29-SEP-2000
29-SEP-2000
29-SEP-2000
02-OCT-2000
02-OCT-2000
02-OCT-2000
02-OCT-2000
13-OCT-2000
13-OCT-2000
20-OCT-2000
20-OCT

2000US-0241808. 2000US-0241809. 2000US-0241826.

2000US

-0246475

2000US-0244617. 2000US-0246474.

2000US-0241786 2000US-0241787

2000US-0241221 2000US-0241785

2000US 2000US-0239935

-0240960

2000US-023703

005-0236802 Sno 005-0236368 005-0236369

ōus. Suo.

2000US-0246476 2000US-0246477 2000US-0246523 2000US-0246524 2000US-0246524 2000US-0246526 2000US-0246526 2000US-0246527 2000US-0246527 2000US-0246527 2000US-0246532 2000US-0246610 2000US-0246610 2000US-0246611 2000US-0246611 2000US-0246611

0;

```
RESULT
AAU23244
     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
14-AUG-2000
118-AUG-2000
22-AUG-2000
22-AUG-2000
22-AUG-2000
23-AUG-2000
30-AUG-2000
01-SEP-2000
01-SEP-2000
01-SEP-2000
01-SEP-2000
01-SEP-2000
05-SEP-2000
05-SEP-2000
                                                                                                                                                                                                                        14 - AUG
14 - AUG
                                                                                                                                                                                                                                                          14 - AUG-
14 - AUG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase; ligase; hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; neurological disorder; metabolic disorder; inflammatory disorder; cardiovascular disorder; reproductive disorder; blood-related disorder; infectious disorder; cytostatic; anti arthritic; nephrotropic; anticoagulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU23244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200155301-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU23244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human
                                                                                                                                                                                                                                                                                                                              14 - AUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-JUL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-MAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAR-2000
                                                                                                                                                                                                                                                                                                                                              14 - AUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43
                                                                                                                                                                                                                                                                                                                                                                                                  -AUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YAM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDGFYTMENSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens.
                                                                                                                                                                                                                                                                          2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       enzyme polypeptide
2000US-022964

2000US-0224518

2000US-0224519

2000US-0225213

2000US-0225266

2000US-0225266

2000US-0225266

2000US-0225276

2000US-0225276

2000US-0225757

2000US-0225757

2000US-0225757

2000US-0225759

2000US-02259344

2000US-0229344

2000US-0229345
                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0214886.
2000US-0215135.
2000US-021647.
2000US-0216880.
2000US-0217487.
2000US-0217496.
2000US-02174990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0189874.
2000US-0190076.
2000US-0198123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0180628.
2000US-0184664.
2000US-0186350.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001WO-US01239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0205515
2000US-0209467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #330.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A
     29-SEP-2000
29-SEP-2000
29-SEP-2000
02-OCT-2000
03-NOV-2000
06-NOV-2000
08-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-SEP-2000

08-SEP-2000

08-SEP-2000

08-SEP-2000

08-SEP-2000

08-SEP-2000

08-SEP-2000

08-SEP-2000

11-SEP-2000

11-SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-SEP-2000;
29-SEP-2000;
                2000US-0241808
2000US-0241809
2000US-0244617
2000US-0246474
2000US-0246476
2000US-0246476
2000US-0246477
2000US-0246523
2000US-0246524
2000US-0246524
2000US-0246526
2000US-0246527
2000US-0246527
2000US-0246528
2000US-0246610
2000US-0246611
2000US-0246611
2000US-0246611
2000US-0246611
2000US-0246611
2000US-0249211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0230437.
2000US-0230438.
2000US-0231242.
2000US-0231243.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0236370.

2000US-0236802.

2000US-0237037.

2000US-02377038.

2000US-02377040.

2000US-0237935.

2000US-0239935.

2000US-0239937.

2000US-02399360.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0241785.
2000US-0241786.
2000US-0241786.
2000US-0241787.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0234997
2000US-0234998
```

```
RESULT
ABB71549
ID ABB7
XX
AC ABB7
                                                                                                                                                                            В
                                                                                               δ
                                                                                                                      Matches
                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                       metabolic disorders (e.g. phenylketonuria), including the control of the invention can also be used in gene therapy.
                                                                                                                                                                                                                                                                                              The present invention relates to the isolation of novel human enzyme polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wide range of disorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders: (e.g. AIDS) autoimmune disorders (e.g. arthritis), neurological disorders (e.g. AIDE) autoimmune disorders (e.g. phenylketonuria), inflammatory disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-DEC
05-DEC
05-DEC
06-DEC
08-DEC
 ABB71549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC
                      ABB71549 standard; Protein; 306
                                                                                                                                                                                                           Note: The sequence data for this patent did specification, but was obtained in electron:
                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-NOV-
                                                                           45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -NOV-
                                                                                                N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -NOV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -NOV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -NOV-2000
                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences.
                                           9
                                                                           | ||:|| |:|
ssgfhtmmnad
                                                                                                SDGFYTMENSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001-465566/50
                                                                                                                     Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID No 1240; 1180pp; English
                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200105-0259678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0251990.
2000US-0254097.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0251989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0251868.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0256719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   000US-0251856
                                                                           55
                                                                                               12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SC,
                                                                                                                               48.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ruben
                                                                                                                               Score 39; DB Pred. No. 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MS
                      8
                                                                                                                    Mismatches
                                                                                                                                                                                                          electronic
                                                                                                                                          22;
                                                                                                                                                                                                                      not
                                                                                                                    2;
                                                                                                                                                                                                        format directly
                                                                                                                                          Length 146;
                                                                                                                    Indels
                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancerous
                                                                                                                   Gaps
                                                                                                                   0;
밁
                                                                                                                                                                                                                              δÃ
                                                                                                                                                               AAG06340
                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                     Matches
                                                                                                                              AAG06340;
                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Venter
                                                                                                                                                                         10
```

```
The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of
Arabidopsis thaliana
                                         Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                    Arabidopsis thaliana protein fragment SEQ ID NO: 3079
                                                                                                              17-OCT-2000
                                                                                                                                                                      AAG06340 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                               insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB07737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genes from Drosophila
interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-656860/75.
N-PSDB; ABL15652.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAR-2002
                             termination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                         3 DGFYTMENSDRR 14
:| | ||::|||
21 ngsypmedtdrr 32
                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JC,
                                                                                                                                                                                                                                                                                                  Similarity 58. 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  melanogaster
                               sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NO 41439;
                                                                                                                                                                                                                                                                                                               48.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ľ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                                      387
                                                                                                                                                                                                                                                                                                  Score 39; DB
Pred. No. 1.1e
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ
                                                                                                                                                                                                                                                                                               DB 22;
1.1e+02;
2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41439
                                                                                                                                                                                                                                                                                                                            Length 306;
                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention
alling and
                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15
```

0;

```
Title:
Perfect score:
Sequence:
                                                                                                                                            Result
                                                                                                                                                                                                                                                                                                                                                                                           Minimum
Maximum
                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Watch 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                              Database
                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OM protein -
                                                                                                                                      ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90.:
                                                                                                                                                                            score
and is
                                                                                                                                                                                                                                                                                                                                                                                           DB
BG
                                                                                                                                    Score
    41.5
                                                                                                                                                                       d. No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                  seq
                   4422443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                          length: 0
length: 2000000000
                                                                                                                                    Query
    100.0
48.9
47.8
47.8
47.8
47.8
46.7
46.7
46.7
                                                                                                                                                                                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-647-522-2
90
                                                                                                                                                                                                                                                                                                                                            SPTREMBL_19:*
                                                                                                                                                                                                                                                                                                                                                                                                                               562222 seqs, 172994929 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   June 10, 2002, 15:29:16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GNAEHVASAVENANRVNK 18
                                                                                                                                                                                                                                                                       sp_phage:*
                                                                                                                                                                                                                                                                                                                                   sp_archea:*
                                                                                                                                                                                                                                                                                              sp_mammal:*
                                                                                                                                                                                                                                                                                                      sp_invertebrate:*
                                                                                                                                                                                                                                                                                                              sp_human:*
                                                                                                                                                                                                                                                                                                                     sp_fungi:*
                                                                                                                                                                                                                                                                                                                             sp_bacteria:*
                                                                                                                                                                                                        sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                                                                                                                               sp_organelle:*
                                                                                                                                                                                                                                                                                        sp_mhc:*
                                                                                                                                                                                                                         sp_rvirus:*
                                                                                                                                                                                                                               sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                                sp_virus:*
                                                                                                                                                                                                                                                       sp_rodent: *
                                                                                                                                                                                                                                                                sp_plant:*
                                                                                                                                    Length DB
   450
471
654
461
676
676
814
814
811
171
177
177
312
312
312
312
312
312
312
312
312
313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>0</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version 4.5
(c) 1993 - 2000 Comp
  16
16
                          55222226
         Q98KR2
O02776
                                                                                    Q9GV72
Q04928
Q89645
Q98QL5
Q9V5Y9
                                085625
Q9VM45
                                                                     Q92I17
Q59129
                                               Q9F807
P71214
                          Q960D9
                                                                                                                                    ij
                                                               Q93NH5
  Q9KL63
                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search time 58.44 Seconds (without alignments)
53.284 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                562222
Q9vm45 drosophila
Q960d9 drosophila
Q98krz rhizobium 1
Q02776 bos taurus
Q9kl63 vibrio chol
                                                            Q9v5y9 drosophila
Q92i17 rickettsia
Q59129 arthrobacte
Q59nh5 arthrobacte
                                    Q9f807 erwinia amy
P71214 escherichia
085625 escherichia
                                                                                                  Q9gv72 carybdea ra
Q04928 methanother
Q89645 barley yell
                                                                                                                                 Description
                                                                                           Q89645 barley yel.
Q98q15 mycoplasma
                                                     B
                                                                    Š
                                                                                                                                                                                                                                                                                            RESULT
Q9GV72
                                                                                                                          Q9GV72
Q9GV72;
                                                                                                                                                                                                              Carybdea.
                                                                                                                                                                Nakajima T.,
                                                                                                                                                                                                                                       CRT -
                                                                                                                                                                                                                                             TOXIN-1.
                                                      250
                               2
```

ω			ū	41
26	12 Q91A26	1363	45.6	41
Q9qaq8 bovine			5	41
Q9qar5			5	41
066291			5	41
Q66290			<u>ب</u>	41
086623			5	41
Q9qd01			5	41
266199			5	41
Q83331			5	41
			5	
Q9ikd1 rat			5	41
			5	41
Q9j3e7 murine			5	41
039227			•	41
Q9j3f1			ū	41
Q9wr70			<u>ب</u>	41
Q934g0 pseudomonas	_		ŗ	41
069256 bacillus	_		5	41
 Q9f4b6 bacillus 	_		ŗ	
Q9jua4 neisseria			5	
			5	
Q9fss2 oryza			5	41
Q905s9		•	•	41
Q9uit2 homo	_		6	٠
095937 homo	_		6	•
Q9p1s8 homo	_		•	41.5
095769 homo	4 095769		σ.	٠
Q9uitl homo	T.T.T.	4 O L	٠	•

ALIGNMENTS

```
RESULT
Q04928
ID Q0
AC Q0
DT 01
                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 18; Conserv
Q04928 PRELIMINARY; PRT; Q04928; 01-NOV-1996 (TrEMBLrel. 01, Created)
                                                                                                                                                                                                                                                                             Biochem. Biophys. Res. Commun. 275:582-588(2000).
EMBL; AB015878; BAB12728.1; -.
SEQUENCE 450 AA; 49392 MW; CD393CF25BEFD2FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=20422301; PubMed=10964707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-CCT-2001 (TrEMBLrel. 18, Last annotation update)
                                                                                                                                                                                                                                                                                                                                   "Novel proteinaceous toxins from the box jellyfish (sea wasp) Carybdea rastoni.";
                                                                                                                                                                                                                                                                                                                                                                                      Nagai H., Takuwa K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Cnidaria; Cubozoa; Cubomedusae; Carybdeidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=78582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carybdea rastonii.
                                                                                                                                               1 GNAEHVASAVENANRVNK 18
                                                                                                                            GNAEHVASAVENANRVNK 267
                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                       Nakao
                                                                                                                                                                                                                                                                                                                                                                                    M., Ito E., Miyake M.,
                                                                                                                                                                                            0;
                                                                                                                                                                                                         Score 90; DB 5;
Pred. No. 2.3e-06;
                                                                                                                                                                                            Mismatches
                                       471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     450
                                       B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ₽
                                                                                                                                                                                                                           Length 450;
                                                                                                                                                                                                                                                                                                                                                                                      Noda M.,
                                                                                                                                                                                            Indels
                                                                                                                                                                                            0
                                                                                                                                                                                           Gaps
```

0

```
OR SOLUTION OF THE PROPERTY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996
01-NOV-1996
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q89645;
Q89645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDLINE-91108372; PubMed=2273382;

Vincent J.R., Ueng P.P., Lister R.M.,

"Nucleotide sequences of coat protein
barley yellow dwarf virus and their re
coat protein sequences.";

J. Gen. Virol. 71:2791-2799(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barley yellow d
Viruses; ssRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Distribution and characterization of plasmid-related sequence chromosomal DNA of thermophilic Methanobacterium strain."; Mol. Gen. 6enet. 240:81-91(1993).
EMBL; X69114; CAA48867.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=93341463; PubMed=8393514;
Noelling J., Van Eden F.J.M., de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Archaea; Euryarchaeota; Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TremBLrel. 01, Last sequence update)
01-DEC-2001 (TremBLrel. 19, Last annotation update)
(CSM3) PLASMID-RELATED CHROMOSOMAL DNA SEQUENCE CFR-II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=145262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Methanothermobacter thermautotrophicus.
                                                                                                                                                                                                                                         Beckett R.J., Vincent J.R., Submitted (NOV-1993) to the EMBL; D10206; BAA01053.1; -. EMBL; L25299; AAA42868.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                           Larkins B.A., Lister R.M., Vincent J.R.;
"Nucleotide sequence analysis and genomic
isolate of barley yellow dwarf virus.";
J. Gen. Virol. 72:2347-2355(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                   InterPro; IPR000382; Luteo_ORF2.
InterPro; IPR000382; Luteo_ORF2: 1.
Pfam; PF02122; Luteo_ORF2: 1.
PRINTS; PR00913; LVIRUSORF2.
SEQUENCE 654 AA; 70566 MW; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE-92013950;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          325
                                                                                                                                                                                                                   MEROPS; S52.001;
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=12039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Luteovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 NAEHVASAVENANRVN 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NASAVSSAVDDSNSVN 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF01345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  yellow dwarf virus (isolate NY-RPV) s; ssRNA positive-strand viruses, no
  Similarity
10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR001434; DUF11.
1345; DUF11; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 (TrEMBLrel. 01, 6 (TrEMBLrel. 01, 11) (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        471 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=1840612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51595 MW; · 44B8DB34FAB57BDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48.98;
                             55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Methanobacteriales;
                        . 6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                        Lister R.M., Miller W.A.;
EMBL/GenBank/DDBJ databases.
Score 44; DB 12
Pred. No. 1e+02;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     de Vos W.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                        53D5E868926D3D28 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            relationships
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Larkins B.A.;
genes for three isolates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            organization
                                                 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BYDV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Methanobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRC64
                                                 Length 654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            other luteovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Luteoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            0f
                                                                                                                                                                                                                                                                                                                                                                                                                                                            the NY-RPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
  0;
```

.,

Gaps

```
RESULT
Q98QL5
                                                                                                                                                                                                                                                                                                                                         RESULT
Q9V5Y9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20
  RRAPPOCCOCCARA
                                                                                                                                                                                                                                                                                                                                                                                              Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                     οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 8
                                                                                                                                                                                                                                                                        01-MAY-2000
01-MAY-2000
01-DEC-2001
SEQUENCE FROM N.A.
STRAIN-BERKELEY;
MEDLINE-20196006; pubMed=10731132;
MEDLINE-20196006; pubMed=10731132;
Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beesson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
                                                                                                                                                                                                    Eukaryota;
Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-CCT-2001 (TrEMBLrel. 18, Created)
01-CCT-2001 (TrEMBLrel. 18, Last sequence update)
01-CCT-2001 (TrEMBLrel. 18, Last annotation update)
ABC TRANSPORTER XYLOSE-BINDING LIPOPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q98QL5;
                                                                                                                                                                                                                                                            CG13204 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycoplasma pulmonis. Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AL445564; CAC13519.
MypuList; MYPU_3460; -.
InterPro; IPR003760; Bmp.
Pfam; PF02608; Bmp; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chambaud I., Heilig R
Moszer I., Dybvig K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=UAB CTIP; MEDLINE=21267165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MYPU_3460.
                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                               CG13204.
                                                                                                                                                                                                                                                                                                               Q9V5Y9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycoplasma pulmonis.
Nucleic Acids Res. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycoplasmataceae;
                                                                                                                                                                             NCBI_TaxID=7227;
                                                                                                                                                                                          Ephydroidea;
                                                                                                                                                                                                                                                                                                                              Q9V5Y9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3lanchard A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=2107;
                                                                                                                                                                                                                                                                                                                                                                                              441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The complete genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  458 GNGKAAASAVTNAAAANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ш
                                                                                                                                                                                                                                                                                                                                                                                                                     1 GNAEHVASAVENANR 15
                                                                                                                                                                                                                                                                                                                                                       U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GNAEHVASAVENANRVNK
                                                                                                                                                                                                                                                                                                                                                                                              GDLEHLKSIVQKANR
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteome.
461 AA;
                                                                                                                                                                                                      Neoptera;
                                                                                                                                                                                                                                                                        ) (TrEMBLrel.
) (TrEMBLrel.
L (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                         Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  es. 29:2145-2153(2001).
CAC13519.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=11353084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R., Ferris S., Barbe V., S:
., Wroblewski H., Viari A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51096
                                                                                                                                                                                                                                                                                                                                                                                                                                                             47.8%;
53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus/Clostridium
                                                                                                                                                                                                                                                                        13,
19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MW;
                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ω
··
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the murine
                                                                                                                                                                                                                                                                                                                              .PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6724D4D820809CE4
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 16;
1e+02;
                                                                                                                                                                                                                                                                                                                              ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         group; Mollicutes;
                                                                                                                                                                                                                                                                         update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        respiratory pathogen
                                                                                                                                                                                                      Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Samson D., Galisson ., Rocha E.P.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ή
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
```

```
Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum
Maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41
       length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         June 10, 2002, 15:29:41; Search time 18.65 Seconds (without alignments) 37.370 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-647-522-2
90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105224 seqs, 38719550 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gapop 10.0 ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SwissProt_40:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GNAEHVASAVENANRVNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
       11235
11363
11363
11363
11363
11363
11363
11363
11363
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
113776
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
113776
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
11376
1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GenCore version 4.5 (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gapext 0
AXZA_PAAOJ
TPIS_EMENI
PACA_BPP1
FACA_BPP1
FACA_BCTTH
FACA_BACST
FACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105224
                                      P25194
P225194
P226003
002385
0029003
P56817
0026885
P16171
012846
012846
012846
012846
012846
012846
012846
012846
012846
012846
012846
012846
012846
012846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P40820 bacteriopha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P44096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P04828
7 saccharomyc
2 claviceps p
4 methanobact
4 solanum tub
1 lycopersico
                                                                                                                                                                              bovine coro
bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                phaseolus a emericella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bacteriopha
haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human coron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coro
```

O G G D D D D D D D D D D D D D D D D D	A R	Qy Db		SFIDDE			R 0 0 0 9		Z I V R			
	SU 2A	93 6	Query Match Best Local Matches		This between the use modi enti	SEQU MEDI Lehn "Bac			09		237 244 244 27 27 27	ט גי 4 7
01-OCT-1993 (Rel 01-OCT-1993 (Rel 01-OCT-2001 (Rel 16-OCT-2001 (Rel Auxin-induced pr AUX22A OR ARG3 Phaseolus aureus	2 U PHAAU	5-5	Match Jocal Simi	EMBL; X5695 PIR; S18824 PIR; C41045 NON_TER SEQUENCE	een the Europea by no fied an ties reend an	ENCE FR INE-920 herr H. terioph late ge acterio CAUTION	eriopha ses; ds _TaxID=	01-FEB-1995 01-FEB-1995 01-FEB-1995 PAC cutting	1 _BPP1			3 8 8
→ α	STA	ASAVENANRVNK :: SAAVENAKRQNK	ilarity Conserv	1; CAA4 ; S1882 ; C4104 142 142 AA;	This SWISS-PROT entry between the Swiss Ins the European Bioinform use by non-profit modified and this state entities requires a lift or send an email to lift.	OM N.A. 11417; , Guido, age Pl ne expr 1. 173: : IT IS	ge P1. DNA vir 10678;	(Rel.	w		**************************************	22
, Cre , Las , Las n 22 n 22 n be	TANDARD;	18 105	47.8% 69.2% vative	0267.1; 4. 5. 142 16529	Institute Institute formatics t institut statement a license o license(PubMed=1 lin A., gene 10 ession. 6438-64,	uses, no	31, Crea 31, Last 31, Last (GP9)	TANDARD;		345 409 417 1440 1461 1761 1716 1716 1716 1716 1716 1717	ω ~1
ted) sequen annota (Indole n) (Vig	PRT;		s; Score 43 s; Pred. No 2; Misman	v; c5	copyright. It is the of Bioinform is not tute. It the not removes a greenent (% a greenenent (% a greenenenenenenenenenenenenenenenenenene	SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE-92011417; PubMed-1917870; Lehnherr H., Guidolin A., Arber W.; Lehnherr H., Guidolin A., Carber W.; "Bacteriophage P1 gene 10 encodes a t. for late gene expression."; J. Bacteriol. 173:6438-6445(1991)!- CAUTION: IT IS UNCERTAIN WHETHER!	RNA staç	Created) Last sequence Last annotati P9) (Fragment)	PRT;	ALIG	TRPD_AERPE Y148_MYCGE AATC_YEAST MESJ_BUCAI TRME_HELPJ TRME_HELPJ TRME_HELPJ TRME_HELPJ TRME_HELPJ TRME_HELPJ TRME_HELPJ TRME_HELPJ PEP_DROME HOX1_HALRO RA50_THEMA ORC1_HUMAN	
odate) update) cetic ac	194 AA.		43; DB 1; NO. 3.4; smatches		t is p format The Iong moved. (See h).	rans-act	je; Caudovirale	e update) ion update)	142 AA.	ALIGNMENTS	RRPE CAST CAST LLPJ LLPJ LLPJ EMAN	BCH
id induced			Length 14 2; Indels	7 CRC64;	roduced through a ics and the EMB: ics and the EMB: re are no restrict as its content its usage by and http://www.isb-sil	vat	ss.	,			00770077708	0 Q
protes			12;		ugh a c EMBL estrict it is and fo sb-sib.	tor re	Myoviridae		:		Q9y8t2 a p47394 m p47394 m p23542 s p57211 b Q9zjg6 h Q25991 n p241073 d p2468 h Q9x1x1 t Q9x1x1 t	0 <
ein ARG3).		•	Gaps		a collaboration BL outstation ictions on its is in no way for commercial ib.ch/announce/	required	ř				rum asm rom bac bac bac hil hil nth	dbrio cho
			0;		its way ercial	1 1 1 1					tte ta a a a a a a a a a a a a a a a a a	b O

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```
RESULT
    CCCCCCCCCRRRRRRRRRR OOCCGDD DD AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yamamoto K.T., Mori H., Imaseki H.;

"CDNA cloning of indole-3-acetic acid regulated gene
from mung bean (vigna radiata) hypocotyl tissue.";

Plant Cell Physiol. 33:93-97(1992).

-! FUNCTION: COULD ACT AS REGULATOR OF GENES RESPON
MEDIATING THE VARIOUS AUXIN-INDUCED EVENTS RESPON
GROWTH (BY SIMILARITY).

-! SUBCELLULAR LOCATION: Nuclear (By similarity).

-! DEVELOPMENTAL STAGE: FOUND IN ELONGATING HYPOCOT
-! INDUCTION: BY AUXIN AND CYCLOHEXINIDE.

-! SIMILARITY: BELONGS TO THE AUX/IAA FAMILY.
                                                                                                                                                                                                                                                                                                                                 TPIS_EMENI STAI

P04828;

13-AUG-1987 (Rel. (

13-AUG-1987 (Rel. (

01-FEB-1996 (Rel. (
                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-86245050; PubMed=3521890;
MCKnight G.L., O'Hara P.J., Parker M.L.;
"Nucleotide sequence of the triosephosphate
Aspergillus nidulans: implications for a dif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D14412; BAA03308.1; -.
InterPro; IPR003311; AUX_IAA.
'Pfam; PF02309; AUX_IAA; IAA.
Multigene family; Nuclear protein; Translation r
SEQUENCE 194 AA; 21514 MW; BBE3BC6D925FC88C
  the
                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                Emericella nidulans (Aspergillus nidulans).
Eukaryota; Fungi; Ascomycota; Pezizomycotin
Eurotiales; Trichocomaceae; Emericella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                        Cell 46:143-147(1986)
                                                                                                                                                                                                                                                                                                                                                                                                             EMENI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Hypocotyl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                       -
                                                                                                                                                                                                                                                   NCBI_TaxID=5072;
                                                                                                                                                                                                                                                                                                                      Triosephosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna. NCBI_TaxID=3916;
                                                                                                                                                        introns."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N
European
by non-
                                                                 SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY
                                                                                    PATHWAY: PLAYS AN IMPORTANT SUBUNIT: HOMODIMER.
                                                                                                                         CATALYTIC ACTIVITY:
                                                                                                            prosprate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DAEHVAVANKNGEKKNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAEHVASAVENANRVNK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
              Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                       isomerase
                                                                                                                                                                                                                                                                                                                                    . 05, Created)
. 05, Last sequence 33, Last annotations.
                                                                                                                                                                                                                                                                                                                    Last sequence of Last annotation Last annotation (EC 5.3.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47.8%;
52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               35
                                                                                                                        D-glyceraldehyde
                                                                                                                                                                                                                                                                a; Pezizomycotina;
Emericella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 43; DB
Pred. No. 4.8;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ω
••
                                                                                              ROLE
                                                                                                                                                                                                                                                                                                                    tion .1.1)
                                                                                                                                                                                                                                                                                                                                                 update)
long
                                                                                              N
                                                                                                                                                                                                                                                                                                                                                                                          249
                                                                                                                                                                                                                                                                                                                    update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4 . 8;
             There are
                                                                                              SEVERAL
                                                                                                                        3-phosphate =
                                                                                                                                                               ate isomerase
differential
                                                                                                                                                                                                                                                                                                                                                                                          Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ۲.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOCOTYLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESPONSIBLE I
                                                                                                                                                                                                                                                                            Eurotiomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      regulation
C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genes: Aux22 and
                                                                                              METABOLIC
             no restrictions
content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 λq
                                                                                                                                                                  gene
loss
                                                                                                                        glycerone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FOR
E FOR
                                                                                              PATHWAYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         is for
                                                                                                                                                                from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in no way commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAUR
          on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
```

```
RESULT 4
                Qy
                                                                                             망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ν.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Ma
Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; D10019; BAA00908.1; PIR; A25502; ISASTN. HSSP; P00940; BTIM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not remove entitles requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                   EMBL; M74046; PIR; S21780; S
                                                                                                                                                 or send
                                                                                                                                                                       modified
                                                                                                                                                                                                                                   "Bacteriophage P1 genes involved in the recognition and cleavag the phage packaging site (pac).";
J. Mol. Biol. 223:977-989(1992).
-i- FUNCTION: NECESSARY FOR RECOGNITION AND CLEAVAGE OF THE PHAPACKAGING SITE (PAC), TOGETHER WITH THE PACB PROTEIN. BOTH PROBABLY THE TWO MAJOR SUBUNITS OF THE PHAGE PACASE.
-i- SUBUNIT: MULTIMER OF TWO DISTINCT SUBUNITS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=92167273; PubMed=1538406;
                                                                                                                                                                                                                                                                                                                                                                     Bacteriophage F
Viruses; dsDNA
                                                                                                                                                                                                                                                                                                                                                                                                    Terminase A
                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-1992
01-DEC-1992
                                                                                             SEQUENCE
                                                                                                       Hydrolase;
                                                                                                                                                                                            the
                                                                                                                                                                                                      between
                                                                                                                                                                                                                  This
                                                                                                                                                                                                                                                                                                                 Skorupski K., Pierce
                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10678
                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                               P28813
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PACA_BPP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD001005; Trioseph_isomrse;
PROSITE; PS00171; TIM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pentose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      somerase;
93
                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 GNAESTTSIIKNLNSAN
                    6
                                                               Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GNAEHVASAVENANRVN
                                                                                                                                                                                s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no rest by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
            VASAVENANRVNK
VSAAVENAKRONK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF00121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           shunt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
8; Conserv
                                                                                                                                                 an email to license@isb-sib.
                                        Similarity 69.
9; Conservative
                                                                                                                                              non-profit institutions we and this statement is not removed and this statement is not removed. requires a license agreement (See
                                                                                            Nuclease;
397 AA; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94
166
249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycolysis; Gluconeogenesis;
                                                                                                                                                                                                                                                                                                                                                                           (Rel. 24, Createq)
(Rel. 24, Last sequence update)
(Rel. 24, Last annotation update)
(Rel. 24, Last annotation update)
A protein (PACASE A protein) (DNA packaging A protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                  S21780
                                                                                                                                                                                                                                                                                                                                                                  P1.
NA viruses,
                                                                                                                             AAA21723.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94
166
27157 -
105
                     18
                                                   47.8%;
69.2%;
                                                                                             45279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47.8%;
47.1%;
                                                                                          DNA-binding.
45279 MW; 247B64DE3EE2D550
                                                                                                                                                                                                                                                                                                                 J.C., Sauer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Trioseph_isomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17
                                                                                                                                                                                                                                                                                                                                                                      no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M.
                                                                                                                                                                                                                                                                                                                                                                     RNA stage; Caudovirales; Myoviridae
                                        Score 43; DB Pred. No. 10; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43; DB Pred. No. 6.2; 2; Mismatches
                                         2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03AF1BA27B545A1C
                                                                                                                                                                                                                                                                                                    in'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        removed
                                                                                                                                                                                                                                                                                                    the recognition
                                                                                                                                                                                                                                                                                                                                                                                                                                                         397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fatty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
                                                              1.
                                                                                                                                                           http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.isb-sib
                                                                                                                                                                      Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Usage
                                         2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acid biosynthesis;
                                                             Length 397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 249;
                                                                                             CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                       ρy
                                                                                                                                                                                                                                                                                                     and cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bу
                                                                                                                                                                                           restrictions
                                                                                                                                                                        and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and
                                                                                                                                                                                                      EMBL
                                                                                                                                                                                                                                                         HE PHAGE
BOTH ARE
                                                                                                                                                                                   ı.
                                                                                                                                                                                                     a collaboration - MBL outstation -
                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .ch/announce/
                                                                                                                                                                                   'n
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                      Off.
                                                                                                                                                                                 0 On
                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
```

```
RESULT
ABGB_EC
ID AI
AC PI
DT 10
DT 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
YAJQ_H
                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                    δÃ
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local s
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YAJO_HAEIN
P44096;
01-NOV-1995
01-NOV-1995
16-OCT-2001
                                                                                     P76052;
16-OCT-2001
16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                     ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fleischmann R.D. Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Witterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Langen H., Takacs B., Evers S., Berndt I
Gray C., Fountoulakis M.;
"Two-dimensional map of the proteome of
Electrophoresis 21:411-429(2000).
-!- SIMILARITY: STRONG, TO E.COLI YAJQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=RD / KW20 / ATCC 51907;
MEDLINE=95350630; Pubmed=75428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U32784; AAC22694.1; TIGR; HI1034; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                         Escherichia
                                              Aminobenzoyl-glutamate ABGB OR B1337.
                                                                                                                                                                                 ABGB_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDENTIFICATION BY MASS SPECTROMETRY. MEDLINE-20137488; PubMed-10675023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Whole-genome random sequencing influenzae Rd.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HI1034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein HI1034.
                                                                                                                                                                                                                                                                                             15
                                                                                                                                                                                                                                                                                                                                    6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                             VRNAVENANRV
                                                                                                                                                                                                                                                                                                                                      VASAVENANRV 16
                                                                                                                                                                                                                                                                                                                                                                                  Similarity 81.09; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             non-profit institutions as long
and this statement is not removed.
requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteome.
Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163
                                                                                       Rel. 40,
1 (Rel. 40,
1 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         influenzae
                           col i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                             25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32,
40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed-7542800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18551 MW;
                                                                                                                                                                                                                                                                                                                                                                                                       46.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last
Last
                                                                                       Last sequence update)
Last annotation updat
                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                     utilization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gamma
  gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence u
                                                                                                                                                                                                                                                                                                                                                                                  Score 42; DB 1;
Pred. No. 5.8;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1831F75A887A4717 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Berndt P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and assembly of Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    subdivision; Pasteurellaceae,
                                                                ion update)
protein B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163
                                                                                                                                                                                 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haemophilus influenzae.";
                                                                                                                                                                              A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lahm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Usage
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          H.W., Wipf
                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ьy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                  0
```

밁

2 NAEHVASAVENA

50 13

δÃ

SMOO_HUMAN RESULT

SMOO_HUMAN

STANDARD;

PRT;

915

₿

P53814; 000569; 01-OCT-1996 (Rel 15-DEC-1998 (Rel 16-OCT-2001 (Rel

(Rel. 34, Created) (Rel. 37, Last seq (Rel. 40, Last ann

37, Last sequence update)
40, Last annotation update)

Smoothelin.

Homo sapiens (Human)

NCBI_TaxID=9606 Eukaryota; Metazoa; Mammalia; Eutheria;

Primates;

Catarrhini; Hominidae;

Craniata; Vertebrata; Euteleostomi;

Chordata;

SEQUENCE FROM N.A. (LONG

smooth

)NG FORM).

Submitted TISSUE=Vascular van Eys G.J.J.M

(MAR-1998)

ç

the EMBL/GenBank/DDBJ databases

muscl

(SHORT

PubMed=8707825; L., Schaart G.,

Timmer

E.D.J.,

Ramaekers F.C

van der Loop F.T.L., MEDLINE=96295554; TISSUE-Smooth SEQUENCE FROM N.A.

novel

cytoskeletal protein specific for smooth muscle

```
Query Match
Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia.
NCBI_TaxID=562;
[1]
                                                                                              ECOGene;
                                                                                                                                                                                                                                                           Husseln M.J., Green J.M., Nichols B.P.;

"Characterization of mutations that allow p-aminobenzoyl-glutamate utilization by Escherichia coll.";

J. Bacteriol. 180:6260-6268(1998).

-i- FUNCTION: REQUIRED BUT NOT ESSENTIAL FOR AMINOBENZOYL-GLUTAMATE UTILIZATION. MAY PARTICIPATE IN HYDROLYSIS OF AMINOBENZOYL-GLUTAMATE TO AMINOBENZOATE, EITHER ALONE OR IN COMBINATION WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restr
                                                                    SEQUENCE
                                                                              Complete proteome.
                                                                                                                                      or send
                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99047572;
                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BN101
                                                                                                                                                                                                                                                                                                                                                                                         CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                 "The complete genome sequence Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                   ABGA.
                                                                                              AE000231; AAC74419.1;
ne; EG13351; abgB.
                                                                                                                                      an email to license@isb-sib.ch).
 Similarity
8; Conserv
                                                                   481 AA;
  Conservative
                                                                                                                                                                                                                                                                                                                                                               PubMed=9829935
                                                                    52193 MW;
               46.7%;
Score 42; DB
Pred. No. 18;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                of Escherichia coli K-12.";
                                                                    84B09100A563E07C CRC64;
           . 18;
                                                                                                                                                      (See http://www.isb-sib
                                                                                                                                                                                 as its content
                              ۲,
                                                                                                                                                                  Usage
  0
                            Length 481
    Indels
                                                                                                                                                                                             restrictions
                                                                                                                                                                    and
                                                                                                                                                                                 is
                                                                                                                                                                                                                        a
                                                                                                                                                                    for
  0
                                                                                                                                                                                                              collaboration
                                                                                                                                                      .ch/announce/
                                                                                                                                                                                                             outstation
                                                                                                                                                                                 'n
                                                                                                                                                                    commercia.
                                                                                                                                                                                 8
                                                                                                                                                                                              9
                                                                                                                                                                                way
  0
```

use by modified

non-profit and this st

institutions as

removed.

long

as

its content

18

H

ö

commerc

ial

```
RESULT
VGL2_C
         STATES AND DESCRIPTION OF THE TENERS OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 12
                                                                                                                                                                MEDILING AND IS INVOLVED

Schmidt I, Skinner M.A., Siddell S.G.,

Schmidt I, Skinner of the gene encoding the sequence of the gene encoding the sequence of coronavirus MHV-UHM.";

J. Gen. Virol. 68:47-56(1987)

J. Gen. VIrol. 89:47-56(1987)

J. Gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
E2 glycoprotein precursor (Spike glycoprotein)
[Contains: Spike protein S1 (90B); Spike protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This
                                                               This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      СУМЈН
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Y13492; CAA73884.1; -.
EMBL; Z49989; CAA90281.1; -.
HSSP; Q01082; 1BKR.
MIM; 602127; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VGL2_CVMJH
P11225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00307; CH; SMART; SM00033; CH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; ssRNA
Coronaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Structural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001715;
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-87111467; PubMed-3027248;
                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=11144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. TISSUE SPECIFICITY: SMOOTH MUSCLE; CONTRACTILE OR VASCULAR (
                                                                                           SUBCELLULAR LOCATION: Type I membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: CONTAINS 1 CALPONIN-HOMOLOGY (CH) DOMAIN
      European
SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEPLAAAVEAANGAERARVNK 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AEHVASAVENAN-----RVNK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a compart the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                 THE HOST CELL RECEPTOR AND D IN SYNCYTIUM FORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coronavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LONG FORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PS50021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         708
778
795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  irus MHV (strain
positive-strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            809
901
544
98449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alternative splicing 713 POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Calponin_hom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 1 de
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₩;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 41.5; D
Pred. No. 44;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MISSING (IN SHORT ISOFORM).
338558BB49E3F1B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JHM).
viruses, no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lycoprotein) (Peplomer protein)
Spike protein S2 (90A)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (See http://www
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA
                                                                                                                                                                                                           THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ۲.
                                                                                                                                                                             IN MEMBRANE
                                                                                                                                                                                                                                                                                                surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     stage; Nidovirales
                                                                                                                                                                                                           BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A FILAMENTOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OR VASCULAR (FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ϋ́q
                                                                                                                                                                                                                                                                                          projection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and
                                                                                                                                                                                                           OF VIRIONS
                                                                                                                                                                                FUSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SHOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               n no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
```

õ

```
RESULT
VGL2_CV
                                                                                                                                                                                                             밁
                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                            Matches
                                                                                                                                                            JLT 9
2_CVMA5
VGL2_CVMA5
P11224;
                                                                                                                                            01-JUL-1989
01-FEB-1996
                                                                                                                                                                                                                                                                                                         CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                          CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                             Murine coronavirus MHV (strain Viruses; ssRNA positive-strand Coronaviridae; Coronavirus. NCBI_TaxID=11142;
                                                                                                                                                                                                             1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X04797; CAA28484.1;
EMBL; D00093; BAA00057.1;
PIR; A33095; VGIHMJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removentities requires a license agreement (S or send an email to license@isb-sib.ch).
         Virology 161:479-487(1987)
                      Luytjes W., Sturman L.S., Bredenbeek P.J., Charite J., van der Zeijst B.A.M., Horzinek M.C., Spaan W.J.M.; "Primary structure of the glycoprotein E2 of coronavirus identification of the trypsin cleavage site.";
                                                      SEQUENCE FROM N.A.
MEDLINE=88072088; PubMed=2825419;
                                                                                                                              16-OCT-2001
E2 glycoprot
                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein; Envelope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002552; Corona_S2
Pfam; PF01601; Corona_S2; 2.
                                                                                                                      Contains:
                                                                                                                                                                                                                                                  Local
                                                                                                                    1 GNAEHVASAVENA
                                                                                                                                                                                                             GNGNHILSLVQNA 1017
                                                                                                                                                                                                                                           Similarity 7; Conserv
 HOST
                                                                                                                                                                                                                                                                                   Rel. 11, 6 (Rel. 33, 1 (Rel. 40,
                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                   AA;
PEPLOMER PROTEIN MEDIATES THE RECEPTOR AND IS INVOLVED
                                                                                                                                                                                                                           13
                                                                                                                                                                                                                                                   45.6%;
53.8%;
                                                                                                                                                                                                                                                                                    136653
                                                                                                                                     Last sequence up
                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein;
                                                                                                                                                                                                                                                                                  N-LINKED
N-LINKED
MW; 25962
                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
E2 GLYCOPROTEIN.
SPIKE PROTEIN S1.
SPIKE PROTEIN S2.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                         N-LINKED
                                                                                                                                                                                                                                                                                                                                                                               N-LINKED
N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                              CYS-RICH.
N-LINKED
                                                                                                                                                                                                                                                   Score
Pred
                                                                                                                                                                                                                                                                                                                         N-LINKED
                                                                                                                                                                                                                                                                                                                                                        N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                 N-LINKED
                                                                                                                                                                                                                                                                                                                                                                       N-LINKED
                                                                                                                                                                     PRT;
                                                                                               viruses,
                                                                                                      A59).
                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane;
                                                                                                                                                                                                                                                                                    25962AD6C1F92DD2
                                                                                                                                                                                                                                                   NO.
                                                                                                                                             update)
                                                                                                                                                                     1324
                                                                                                                                                                                                                                                                                                                                (GLCNAC.)
(GLCNAC.)
(GLCNAC.
                                                                                                                                                                                                                                                                                                                (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                               (GLCNAC.
(GLCNAC.
(GLCNAC.
                                                                                                                                     update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (See
                                                                                                                                                                                                                                                                                          (GLCNAC. .
                                                                                                                                                                                                                                                                                                                                                                                                              (GLCNAC.
                                                                                                                                                                                                                                                   DB
73;
                                                                                                                                                                                                                                                                                                                                                        (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                              (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                              (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                       (GLCNAC
                                                                                               o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.isb-sib
                                                                                              DNA stage; Nidovirales;
                                                                                                                                                                                                                                                           ۲
THE B
                                                                                                                                                                                                                                           4;
                                                                                                                      (Peplomer protein)
In S2 (90A)].
                                                                                                                                                                                                                                                           Length 1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal.
         BINDING
MEMBRANE
                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                (POTENTIAL). (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                 MHV-A59
FUSION
                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch/announce/
                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                           0
```

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STITE TO THE TENT OF THE TENT 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                   LT 10
CCVHOC
VGL2_CVHOC
P36334;
                                                                                                                                                                                                                             01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
E2 glycoprotein precursor (Spike glycoprotein) (Peplomer protein)
[Contains: Spike protein S1 (90B); Spike protein S2 (90A)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
CARBOHYD
CARBOHYD
  SEQUENCE FROM N.A.
MEDLINE-93399458; PubMed-8376972;
MOUNIT S., Talbot P.J.;
"Molecular characterization of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A27402; VGIH59.
InterPro; IPR002552; Corona_S2.
Pfam; PF01601; Corona_S2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This
                                                                                                                                                  Viruses; ssRNA
Coronaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1094
                                                                                                                         NCBI_TaxID=31631;
                                                                                                                                                                                                    Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M18379; AAA46455.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND IN SYNCYTIUM FORMATION. SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GNAEHVASAVENA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GNGNHILSLVQNA 1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is
                                                                                                                                                                                             coronavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 53.8
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SS-PROT entry is copyright. It is produced through a copyright the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Envelope
                                                                                                                                                  rus (strain OC43) positive-strand Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ĀΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1324
11324
11285
11285
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
11286
1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45.6%;
53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL
CYS-RICH.

N-LINKED (GLCNAC...)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 41; DB Pred. No. 78; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPIKE PROTEIN S
SPIKE PROTEIN S
EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                            PRT;
     the S
                                                                                                                                                                         viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLYCOPROTEIN
  protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         There are no restrictions ing as its content is in
                                                                                                                                                                      no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N S1.
N S2.
R (POTENTIAL).
                                                                                                                                                                 DNA stage; Nidovirales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ۲,
gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .) (POTENTIAL)
.) (POTENTIAL)
E CRC64;
     of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                γď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
     human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
```

```
RESULT 11
VGL2_CVBF
ID VGL2_AC P2519
AC P2519
DT 01-MA
DT 01-MA
DT 16-OC
DE E2 91
DE (Cont
GN S.
OS BOYIC
OC Virus
OC Coror
                                                                                                                                                           Š
                                                                                                                                           밁
                                                                                                                                                                                                                             Query Match
Best Local S
Matches 7
                        VGL2_CVBF STANDAKU;
VGL2_CVBF STANDAKU;
P25190;
01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
E2 glycoprotein precursor (Spike glycoprotein) (P
                                                                                                                                                                                                                                                                                 CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                            CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                             CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
CARBOHYD
                                                                                                                                           1128
                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Gen. Virol. 74:1981-1987(1993).
-!- FUNCTION: THE PEPLOMER PROTEIN MEDIATES THE BINDING OF TO THE HOST CELL RECEPTOR AND IS INVOLVED IN MEMBRANE AND IN SYNCYTIUM FORMATION.
                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein; SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI
                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L14643; AAA03055.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coronavirus OC43.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002552; Corona_S2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; JQ2168; JQ2168
                                                                                                                                                          1 GNAEHVASAVENA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AND IN SYNCYTIUM FORMATION.
SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                         GNGNHIISLVQNA
                                                                                                                                                                             Similarity
7; Conserv
                                                                                                                                                                                                                            778
927
1184
1214
1224
1224
1243
1257
1257
                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Envelope
1 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corona
                                                                                                                                                                                                                                    1353
757
1353
1298
1318
1353
                                                                                                                                                           13
                                                                                                                                                                                      45.6%;
53.8%;
                                                                                                                                                                                                                            150088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein;
                                                                                                                                                                            Score 41; DB Pred. No. 80; 2; Mismatches
                                                                                                                                                                              <u>ب</u>
                                                                                                                                                                                                                            Œ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
E2 GLYCOPROTEIN.
SPIKE PROTEIN S1
SPIKE PROTEIN S2
                                                                                                                                                                                                                                                                         N-LINKED
                                                                                                                                                                                                                                                                                                                                      N-LINKED
                                                                                                                                                                                                                                                                                                                                                        N-LINKED
N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                                                                                             N-LINKED
                                                                                                                                                                                                                                                      N-LINKED
                                                                                                                                                                                                                                                                                         N-LINKED
                                                                                                                                                                                                                                                                                                    N-LINKED
                                                                                                                                                                                                                                                                                                            N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                        CYS-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                     N-LINKED
                                                                                                                                                                                                                                                                                                                              N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane; Signal.
                                                                                                                                                                                                                           7B1CE3CBDB1A902A
                                                                                                                                                                                                                                                                      (GLCNAC
(GLCNAC
(GLCNAC
(GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                   (GLCNAC)
                                                                                                                                                                                                                                    (GLCNAC
(GLCNAC
                                                                                                                                                                                                                                                                                                                   (GLCNAC
(GLCNAC
(GLCNAC
                                                                                                                                                                                                                                                                                                                                                        (GLCNAC
(GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                               (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                              S1.
                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Usage
                                                                                                                                                                                              Ļength 1353;
                                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL). (POTENTIAL). (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            γď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OF VIRIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUSION
                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        outstation
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                             0
```

Bovine coronavirus (strain F15) Viruses; ssRNA positive-strand Coronaviridae; Coronavirus

viruses,

on

DNA

stage;

(Peplomer protein) ln S2 (90A)].

```
RESULT
VGL2_CV
ID VG
AC P2
DT 01
DT 16
DE E:
GN S
                                                                                                                                                                     δÃ
                                                                                               밁
                                                                                                                             Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                           CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                    CARBOHYD
SEQUENCE
                                                                                                                                                                                            CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                          CARBOHYD
CARBOHYD
      VGL2_CVBL9 STANDARD; PRT; 1363 AA.

P25191;
01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
E2 glycoprotein precursor (Spike glycoprotein) (Peplomer protein)
[Contains: Spike protein S1 (90B); Spike protein S2 (90A)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Boireau P., Cruciere C., Laporte J.;
"Nucleotide sequence of the glycoprotein S gene of bovine enteric
coronavirus and comparison with the S proteins of two mouse hepatitis
                                                                                               1138
                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein; Envelope protein;
                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002552; Corona_S2.
Pfam; PF01601; Corona_S2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D00731; BAA00631.1; -. PIR; A34151; VGIHF1.
                                                               CVBL9
                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        virus strains."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=90171938; PubMed=2155300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=11129;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: THE PEPLOMER PROTEIN
                                                                                                       1 GNAEHVASAVENA
                                                                                                                                                                                                                                                                                                                                                                                                                                   send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: THE PEPLOMER PROTEIN MEDIATES THE BINDING OF VIRIOUS TO THE HOST CELL RECEPTOR AND IS INVOLVED IN MEMBRANE FUSION
                                                                                               GNGNHIISLVQNA 1150
                                                                                                                            Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Virol.
                                                                                                                                                                    937
1194
1224
1234
1253
1267
1288
1363
                                                                                                                                                                                                                                                                                                                        1329
                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71:487-492(1990).
                                                                                                                                                                                                          13
                                                                                                                                    45.6%;
                                                                                                                                                                    150746
                                                                                                                            Score 41; DB Pred. No. 81; 2; Mismatches
                                                                                                                                                                   N-LINKED
MW; 3245C
                                                                                                                                                                                          N-LINKED
                                                                                                                                                                                                          N-LINKED
                                                                                                                                                                                                                                   N-LINKED
                                                                                                                                                                                                                                                   N-LINKED
                                                                                                                                                                                                                                                                  N-LINKED
                                                                                                                                                                                                                                                                                  N-LINKED
                                                                                                                                                                                                                                                                                                                                              POTENTIAL.

E2 GLYCOPROTEIN S1.

SPIKE PROTEIN S2.

SPIKE PROTEIN S2.

EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL)
CYS-RICH.
N-LINKED (GLCNAC. . .)
                                                                                                                                                                                    N-LINKED
                                                                                                                                                                                                                           N-LINKED
                                                                                                                                                                                                                                                                                                  N-LINKED
                                                                                                                                                                                                                                                                                                         N-LINKED
                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane;
                                                                                                                                                                                                                                                                                 (GLCNAC)
                                                                                                                                                                                                                                                                                                        (GLCNAC
                                                                                                                                                                                                          (GLCNAC.
                                                                                                                                                                                                                                   (GLCNAC.
                                                                                                                                                                                                                                                                  (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                           (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                (GLCNAC. .
                                                                                                                                                                                                                           (GLCNAC.
                                                                                                                                                                           (GLCNAC
                                                                                                                                                                                           (GLCNAC
                                                                                                                                                                                                    (GLCNAC.
                                                                                                                                                                                                                                                   (GLCNAC.
                                                                                                                                                                                                                                                          (GLCNAC
                                                                                                                                           1;
                                                                                                                            4;
                                                                                                                                                                                                                                                                                                                                                                                     Signal.
                                                                                                                                           Length 1363
                                                                                                                             Indels
                                                                                                                                                                                                                                                  (POTENTIAL). (POTENTIAL). (POTENTIAL).
                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                    (POTENTIAL
                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                   and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                            is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  מ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VIRIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   for
                                                                                                                             0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                            μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                   in no way
                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           on
                                                                                                                            0,
RESULT
VGL2_CV
ID VC
AC PC
DT 0:
DT 0:
DT 1:
DE E
                                                                                                                                                    멍
                                                                                            20
glycoprotein
```

```
Query Match
Best Local S
Matches 7
VGL2_CVBLY S
P25192; Q9QAS2;
01-MAY-1992 (Rel
01-MAY-1992 (Rel
16-OCT-2001 (Rel
                                                                                                                                                                                      CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                            CARBOHYD
CARBOHYD
CARBOHYD
                                                   CVBLY
                                                                                             1138
                                                                                                                                                                                                                                         CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M64bb,,...
PIR; A40320; VGIHL9.
ThterPro; IPR002552; Corona_S2.
ThterPro; Corona_S2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COTONAVITUSES., -404(1991).
VITOLOGY 183:397-404(1991).
-!- FUNCTION: THE PEPLOMER PROTEIN MEDIATES THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-91272503; PubMed-2053289;
Zhang X., Kousoulas K.G., Storz J
"Comparison of the nucleotide and
S genes specified by virulent and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bovine coronavirus (strain L9).
Viruses; ssRNA positive-strand
Coronaviridae; Coronavirus.
NCBL_TaxID=11130;
                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a continuous the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A MEDLINE-91272503;
                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein;
                                                                                                               1 GNAEHVASAVENA
                                                                                             GNGNHIISLVQNA
                                                                                                                                   7; Conserv
                                                                                                                                                                                       788
937
1194
1224
1234
1253
1267
1363
(Rel.
                                                                                                                                                                                                                                                                                              198
359
437
676
696
714
                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Envelope
1
                                          STANDARD;
                                                                                                                                                                                       AA;
22, Created)22, Last sequence update)40, Last annotation update)
                                                                                                                                                                                                                                                                                  788
937
1194
1224
1234
1234
1253
1267
                                                                                                               13
                                                                                                                                             5 4.
5 5 5
                                                                                                                                                                                       150806
                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein;
                                                                                                                                             . 68
                                                                                                                                                                                      N-LINKED
                                                                                                                                                                                                                                                                                             N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                            SPIKE PROTEIN
SPIKE PROTEIN
EXTRACELLULAR
                                                                                                                                             Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
E2 GLYCOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and
                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane;
                                                                                                                                      Mismatches
                                                                                                                                                                                       INKED (GLCNAC. . INKED (GLCNAC. . SD27D1A58FBFC951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     deduced amino acid
                                           1363
                                                                                                                                                                                                                   (GLCNAC.
(GLCNAC.
(GLCNAC.
                                                                                                                                                                                                                                                             (GLCNAC.
(GLCNAC.
                                                                                                                                                                                                                                                                                                                   (GLCNAC.
                                                                                                                                                                                                                                                                                                                                      (GLCNAC.
(GLCNAC.
(GLCNAC.
                                                                                                                                                                                                                                                                                              (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (See http://www.isb-sib.ch/announce,
                                                                                                                                              81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      no
                                           ₽
                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA
                                                                                                                                                        ۲.
                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IN MEMBRANE E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      stage; Nidovirales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal
                                                                                                                                                        Length 1363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BINDING OF
                                                                                                                                                                                     .) (POTENTIAL)
.) (POTENTIAL)
1 CRC64;
                                                                                                                                                                                                                  (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
                                                                                                                                                                                                                                                                                            (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bу
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of bovine
                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is
for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a collaboration -
MBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VIRIONS
                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ιn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ō,
                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in no way commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    on
                                                                                                                                     0
```

precursor (Spike glycoprotein)

(Peplomer protein)

```
RESULT 14
VGL2_CVBM STANDARD;
ID VGL2_CVBM STANDARD;
AC P15777;
DT 01-APR-1990 (Rel. 14, Created)
                                                                                                                                                                                                                                                                                                                                                                            SPARTE TO THE TERM TO THE TERM
                                                                                                                                                                      Вþ
                                                                                                                                                                                                            δÃ
                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                      1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VIROLOGY 183:397-404(1991).

VIROLOGY 183:397-404(1991).

-I- FUNCTION: THE PEPLOMER PROTEIN MEDIATES THE BINDING OF VIRIONS
TO THE HOST CELL RECEPTOR AND IS INVOLVED IN MEMBRANE FUSION.
                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collabortween the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; C40320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhang X., Kousoulas K.G., Storz J.;
"Comparison of the nucleotide and deduced amino acid sequences
S genes specified by virulent and avirulent strains of bovine."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPRO
Pfam; PF01601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF058942; AAF25499.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coronaviruses."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; ssRNA
Coronaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=91272503; PubMed=2053289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=11131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lycoprotein;
                                                                                                                                                                                                            1 GNAEHVASAVENA 13
                                                                                                                                                                    GNGNHIISLVQNA 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coronavirus (strain LY-138).
s; ssRNA positive-strand viruses,
viridae; Coronavirus.
                                                                                                                                                                                                                                                              Similarity 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR002552; Corona_S2.
                                                                                                                                                                                                                                                                                                                                                                          Spike
                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Envelope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corona_S2;
                                                                                                                                                                                                                                                                                                                                                                          A.
                                                                                                                                                                                                                                                                                                                                                                                             1253
1267
1288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                             53
                                                                                                                                                                                                                                                                                                                                                                       150676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein;
                                                                                                                                                                                                                                                                               8 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S1
                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC.
N-LINKED (GL
                                                                                                                                                                                                                                                  Score 41; DB
Pred. No. 81;
2; Mismatches
                                                                                                                                                                                                                                                          2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    potential.

E2 GLYCOPROTEIN.

SPIKE PROTEIN S1.

SPIKE PROTEIN S2.

EXTRACELLULAR (POTENTIAL STATEMENT S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (90B);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
CYTOPLASMIC (POTENTIAL).
CYS-RICH.
                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spike
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           no DNA stage; Nidovirales;
                                                  Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N S1.
N S2.
R (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as its content i
                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                       4;
                                                                                                                                                                                                                                                                                                Length 1363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S2
                                                                                                                                                                                                                                                                                                                                                                  CRC64;
                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (90A)]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a collaboration
                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of.
                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           commercia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ņ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    its
                                                                                                                                                                                                                                                  0;
```

```
CARBOHYD
CARBOHYD
                                                                                                                                                     CARBOHYD
CARBOHYD
                                                                                                                                                                                                                      CHAIN
CHAIN
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                     CARBOHYD
                                               CARBOHYD
                                                         CARBOHYD
                                                                 CARBOHYD
                                                                            CARBOHYD
                                                                                                       CARBOHYD
                                                                                                                 CARBOHYD
                                                                                                                          CARBOHYD
                                                                                                                                   CARBOHYD
                                                                                                                                             CARBOHYD
                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                 Glycoprotein; Envelope protein; SIGNAL 1 17 PO
                                                                                                                                                                                                                                                                                                                         modified and this statement is not removentitles requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                         Abraham S., Kienzle T.E., Lapps W.E., Brian D.A.; "Sequence and expression analysis of potential no of 4.9, 4.8, 12.7, and 9.5 kDa encoded between the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE=9032743; PubMed=2184576;

Abraham S., Kienzle T.E., Lapps W.E., Brian D.A.;

"Deduced sequence of the bowine coronavirus spike protein identification of the internal proteolytic cleavage site."

"Irology 176:296-301(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1990 (Rel. 14, Last
16-OCT-2001 (Rel. 40, Last
E2 glycoprotein precursor
[Contains: Spike protein S
                                                                                                                                                                                                                                                                    InterPro; IPR002552; Corona_S2.
                                                                                                                                                                                                                                                                                               EMBL; M31053; AAA66399.1;
EMBL; M31054; AAA42910.1;
                                                                                                                                                                                                                                                                                                                                                       use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1254-1363 FROM N.A. MEDLINE=90320120; PubMed=2142556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bovine coronavirus (strain Mebus).
Viruses; ssRNA positive-strand viruses, no
Coronaviridae; Coronavirus.
NCBI_TaxID=11132;
                                                                                                                                                                                                                                                                                      PIR; A34607; VGIHNM.
                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Abraham S.,
                                                                                                                                                                                                                                                                                                                                                       non-profit
 1312
1329
1329
1333
133
198
359
437
649
649
6696
696
697
697
11194
71194
7124
11234
11234
11267
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kienzle T.E., Lapps
                                                                                                                                                                                1363
768
1363
1311
1328
1363
1363
                                                                                            133
133
198
359
437
649
676
                                                                                                                                                                                                                                                                                                                                                    institutions as long as its content
150810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Spike glycoprotein) (Peplomer pr
S1 (90B); Spike protein S2 (90A)].
 ž
                                             N-LINKED
N-LINKED
                                                                                                                                                                                                         POTENTIAL.
E2 GLYCOPROTEIN.
SPIKE PROTEIN S1
SPIKE PROTEIN S2
EXTRACELLULAR (PO
                          N-LINKED
                                                                         N-LINKED
                                                                                                                                          N-LINKED
                                                                                                                                                                                                                                                                                                                                             is not removed.
        N-LINKED
                                                                                             N-LINKED
                                                                                                     N-LINKED
                                                                                                                N-LINKED
                                                                                                                        N-LINKED
                                                                                                                                                              N-LINKED
                                                                                                                                                                        N-LINKED
                                                                                                                                                                                 CYS-RICH
                                                                                                                                                                                         CYTOPLASMIC
                                                                                                                                   N-LINKED
                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                        Transmembrane; Signal
 864B3AE0823
                          GLCNAC.
        (GLCNAC.
                                                                                                                                                                                                                                                                                                                                 (See http://www.isb-sib.ch/announce/
                                                                                                                                                                     (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                between the s.";
                                                                                                                                                                                                                                                                                                                                                           There are no restrictions
                                                                                                                                                                                         (POTENTIAL).
                                                                                                                                                                                                                    S1
S2
                                                                                                                                                                                                          (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA stage; Nidovirales;
                                                                                                                                                                                                                                                                                                                                                                                                 THE BINDING OF VIRIONS ED IN MEMBRANE FUSION.
2F458
                                                                                                                                                                                                                                                                                                                                           Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                        nonstructural the spike and
CRC64;
                         (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                           (POTENTIAL)
(POTENTIAL)
                                                                                                                      (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      site.";
                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                            Ьy
                                                                                                                                                                                                                                                                                                                                             and
                                                                                                                                                                                                                                                                                                                                                                      EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein)
                                                                                                                                                                                                                                                                                                                                                                               a collaboration
                                                                                                                                                                                                                                                                                                                                            for
                                                                                                                                                                                                                                                                                                                                                                                                                                        . proteins
l membrane
                                                                                                                                                                                                                                                                                                                                           in no way commercial
```

Query Match Best Local s Matches 7

Similarity
7; Conser

Conservative

2. Score Pred.

Mismatches

0

Gaps

0

41; No.

DB 81;

1;

Length 1363;

45.6%; 53.8%;

B 63

1 GNAEHVASAVENA 13 || |: | |:|| 1138 GNGNHIISLVQNA 1150

0,

```
RESULT 13

VGL2_CVB0

VGL2_CVB0

STANDARD;

ID VGL2_CVB0 STANDARD;

AC P2513;
DT 01-MX-1992 (Rel. 22, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-CCT-2001 (Rel. 40, Last annottation update)
DE E2 91ycoprotein precursor (Spike glycoprotein) (Peplomer protein)
DE E2 91ycoprotein S1 (90B); Spike protein S2 (90A)].

'Contains: Spike protein S1 (90B); Spike protein S2 (90A)].
ALD DAY OF THE PROPERTY OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-90171910; PubMed=2155283;
Parker M.D., Yoo D., Cox G.J., Babiuk L.A.;
Primary structure of the S peplomer gene of bovine coronavirus and surface expression in insect cells.";
J. Gen. Virol. 71:263-270(1990).
-I- FUNCTION: THE PEPLOMER PROTEIN MEDIATES THE BINDING OF VIRIONS TO THE HOST CELL RECEPTOR AND IS INVOLVED IN MEMBRANE FISION.
                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D00662; BAA00557.1; -.
PIR; A34147; VGIHQU.
InterPro; Ipr003552; Corona_S2.
Pfam; PF01601; Corona_S2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=90171910;
                                                                                                                                                                                                     CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                             CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
CHAIN
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
DOMAIN
                                                                                 CARBOHYD
                                                                                                      CARBOHYD
                                                                                                                       CARBOHYD
                                                                                                                                        CARBOHYD
                                                                                                                                                               CARBOHYD
                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIĞNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein; Envelope protein;
SIGNAL 1 17 PO:
  696
714
739
788
937
1194
1224
1234
1233
1267
1267
1363
                                                                                                                                                                                                     150869
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
MW; 6A6587B07A102B71
                                                                             N-LINKED
N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                              N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
CYTOPLASMIC (POTENTIAL).
CYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                              E2 GLYCOPROTEIN.
SPIKE PROTEIN S1.
SPIKE PROTEIN S2.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane; Signal.
                                                                           (GLCNAC.
(GLCNAC.
(GLCNAC.
(GLCNAC.
(GLCNAC.
(GLCNAC.
                                                                                                                                                                                                                        (GLCNAC.
(GLCNAC.
(GLCNAC.
                                                                                                                                                                                                                                                                                                        (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                (GLCNAC.
                                                                                                                                                                                                     (GLCNAC.
                                                                                                                                                                                                                                                                                     (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of bovine coronavirus and
                  (POTENTIAL)
(POTENTIAL)
                                                                             (POTENTIAL)
                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                           (POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                (POTENTIAL)
                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                        (POTENTIAL)
```

Query Match

45.68;

Score 41;

DВ

۲,

Length 1363

```
멍
              δÃ
                              Best Local Similarity 53.0 Matches 7; Conservative
1138
               \vdash
GNGNHIISLVQNA 1150
       GNAEHVASAVENA
                13
                                       53.8%;
                               2;
                                       Pred. No. 81;
                                Mismatches
                                4;
                                Indels
                                0
                                Gaps
```

Search completed: June 10, 2002, 15:29:42 Job time: 477 sec

```
ş
Search completed: June 10, 2002, 15:21:07 Job time: 167 sec
                                                                                                  В
                                                                                                                                                                      Query Match 45.6%; Score 41; DB 14; Length 180; Best Local Similarity 53.8%; Pred. No. 64; Matches 7; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                          The polypeptide comprises a sequence which is highly conserved among coronaviruses and which is capable of eliciting an immune response. The polypeptide and nucleic acid can be used to produce vaccines which can be used to protect animals against different members of the coronavirus family, e.g. feline infectious peritonitis virus, feline enteric coronavirus; canine coronavirus, swine transmissable gastroenteritis coronavirus; bowlne coronavirus; human coronavirus or avian infectious bronchitis virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 26-27; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Universal corona-virus vaccine - comprising a polypeptide contg. a conserved domain of coronavirus S protein or nucleic acid encoding it
                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1993-386472/48.
                                                                                              || |: | |:||
112 gngnhilslvqna 124
                                                                                                                     1 GNAEHVASAVENA 13
                                                                                                                                                                                                                                                                           180 AA;
                                                                                                                                                                        0;
                                                                                                                                                                        Gaps
                                                                                                                                                                        0,
```

```
Title:
Perfect score:
Sequence:
Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                      Total number of hits satisfying chosen parameters:
                                                                                        Searched:
                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                    Run on:
                                                                                                                                                                                                           US-09-647-522-2
90
                                                                                                                                                                                                                                                           June 10, 2002, 15:22:23 ; Search time 35.61 Seconds (without alignments) 48.571 Million cell updates/sec
                                                                                          283138 seqs, 96089334 residues
                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                       1 GNAEHVASAVENANRVNK 18
                                                                                                                                                                                                                                                                                                                                                                                             GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                          283138 .
```

pir_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	ر. د	4	ω	2	_	NO	Result
41	41	41	41	. 41	4 1	41.5		42	42	42	42	42	42	42	43	43	43	43	43	43	43	43	43	43	44	44	45	90	90016	
45.6	45.6	5		45.6		6		46.7					<u>ი</u>	Ġ	7	٠	47.8	7	47.8	7.	7	7	47.8	7.	48.9	48.9		100.0	March	
1361	1353	1324	1235	590	590	915	353	481	481	481	478	312	312	163	814	676	461	397	297	249	238	221	194	142	Ų	471	4	450	renden	7052+1
2	ᆫ	μ.	_	N	N	N	N	N	N	2	N	Ν	2	N	ш	N	N	N	N	_	N	N	N	N	Ν	2	2	2	. DB	3
S29998	JQ2168	VGIH59	VGIHMJ	C81911	B81104	T09575	A82405	D64883	H85749	A90869	AB3641	в91198	F86044	F64018	139627	C97775	в90555	S21780	138517	ISASTN	F98266	AB3018	T10939	C41045	JQ1241	S30585	AF3302	JC7371	10	;
surface protein -	E2 glycoprotein pr	glycoprotein		nitrate/nitrite se	nitrate/nitrite se	٠	\vdash			hypothetical prote	rate hydr		secreted protein E	conserved hypothet	nicotine dehydroge	acylamino-acid-rel	ransporter	pacB protein - pha	syntaxin - human		thiamin-phosphate	thiamin-phosphate	auxin-induced prot	\Box	ŭ	۳	hetical pro	in - jellyfis	Description	1

ALIGNMENTS

```
N;Alternate names: gene 9 protein (C.Species: phage Pl
C.Species: phage Pl
C;Accession: C41045; S18824
R;Lehnherr, H.; Guidolin, A.; Arber, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: JQ1241
A;Accession: JQ1241
A;Mcsidues: 1-653 <VIN>
A;Cross-references: GB:L25299; NID:g408929; PIDN:AAA42868.1; PID:g408933
A;Experimental source: strain NY-RPV
C;Comment: This virus causes yellowing disease in barley, oats, wheat, r:C;Superfamily: potato leaf roll virus 70K protein
                                                                                                                                                                       RESULT
C41045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N;Alternate names: ORF2 protein
C;Species: barley yellow dwarf virus, BYDV
C;Date: 31-Mar-1992 #sequence_revision 31-1
C;Accession: JO1241
R;Vincent, J.R.; Lister, R.M.; Larkins, B.;
J. Gen. Virol. 72, 2347-2355, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein 5 - Methanobacterium thermoformicicum C;Species: Methanobacterium thermoformicicum C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 10-D C;Date: 30:585 R;Noelling, J.; van Eden, F.J.M.; de Vos, W.M. submitted to the EMBL Data Library, November 1992 submitted: Distribution and characterization of plasmid-related hypothesis and the control of the EMBL Data Library is not the EMBL Data 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Title: Nucleotide sequence analysis and A; Reference number: JQ1240; MUID:92013950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ş
                                                                                                                                                                                                                                                                                       B
                                                                                                                                                                                                                                                                                                                                            Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X69114; NID:g44581; PIDN:CAA48867.1; PID:g44582 C;Superfamily: Methanobacterium thermoformicicum hypothetical protein 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-471 <NOE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                             pac cutting enzyme -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viral replicase 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: S30585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: S30583
                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vincent, J.R.; Lister, R.M.; Lar
Gen. Virol. 72, 2347-2355, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        325 NASAVSSAVDDSNSVN 340
                                                                                                                                                                                                                                                                                          457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25
                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N
                                                                                                                                                                                                                                                                                                                                               1 GNAEHVASAVENANRVNK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GNAEHVASAVENANRVNK 18
                                                                                                                                                                                                                                                                                       GNGKAAASAVTNAAAANK 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAEHVASAVENANRVN 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GNAERDAAAQEAARRITK 42
                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             barley yellow dwarf virus
                                                                                                               phage P1 (fragment)
ene 9 protein
                                                                                                                                                                                                                                                                                                                                                                                                                            48.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48.9%;
56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50.0%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Larkins, B.A.
                                                                                                                                                                                                                                                                                                                                                                                                       ۲.
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-Mar-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genomic
                                                                                                                                                                                                                                                                                                                                                                                                                         DB
35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ДВ
20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ψ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 547;
                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NY-RPV isolate of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rice, maize and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ij
                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chr
```

```
C;Genetics:
A;Gene: arg3
C;Superfamily: a
A; Molecule type: DNA
A; Residues: 1-221 <KUR>
A; Cross-references: GB:AE008689; PIDN:AAL44560.1;
A; Experimental source: strain C58 (Dupont)
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.Title: Bacteriol. 173, 6438-6445, 1991
A.Title: Bacteriophage P1 gene 10 encodes a trans-activating factor required:
A.Reference number: A41045; MUID:92011417
A;Accession: C41045
A;Accession: C41045
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: EMBL:X56951; NID:g406728; PIDN:CAA40267.1; PID:g579080
A;Cross-references: EMBL:X56951; NID:g406728; PIDN:CAA40267.1; PID:g579080
A;Note: it is uncertain whether Met-1 (GTG) or Met-65 is the initiator
C;Genetics:
                                                                                                                                                                                                                                                                                                                         RESULT
AB3018
                                                                                                                                                                                   R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; i; Karp, P.; Romero, P.; Zhang, S. science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        auxin-induced protein aux22 - mung b
C;Species: Vigna radiata (mung bean)
C;Date: 16-Jul-1999 #sequence_revisi
C;Accession: T10939
                                                                                   A;Status: preliminary
                                                                                                      A; Reference number: A; Accession: AB3018
                                                                                                                                   A; Title: The Genome
                                                                                                                                                    A; Authors: Yoo, H.; ster, E.W.
                                                                                                                                                                                                                                                                     C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
                                                                                                                                                                                                                                                                                        thiamin-phosphate pyrophosphorylase [imported] - Agrobacterium C;Species: Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-194 <YAM>
A;Cross-references: EMBL:D14412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Yamamoto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Start codon:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene:
                                                                                                                                                                                                                                                         C; Accession: AB3018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                          19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93
                                                                                                                                                                                                                                                                                                                                                                                                                         N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 VASAVENANRVNK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                          DAEHVAVANKNGEKKNK
                                                                                                                                                                                                                                                                                                                                                                                                                        NAEHVASAVENANRVNK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSAAVENAKRONK 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T10939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the EMBL Data
number: Z17206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 69.
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          auxin-induced protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source: hypocotyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                     e of the 1
AB2577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47.8%;
52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47.8%;
                                                                                                                                   Natural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Library,
                                                                                                                     Natural Genetic PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                          ω
5
                                                                                                                                                                      Biddle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ω
--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         February 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ed. No. 9.7;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aux28
                                                                                                                                                                    P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-Jul-1999 #text_change
                                                                                                                                   Engineer Agrobacterium tumefaciens C58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2
                                                                                                                                                                                                                    Kutyavin,
                                PID:g17742176; GSPDB:GN00187
                                                                                                                                                                                                                                  Chen, L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ū
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                    T . ;
                                                                                                                                                                                                                                    Wood, G.E.; Chen,
                                                                                                                                                                                                                   Levy, R.;
                                                                                                                                                                                                                                                                                                       tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                       (strain
                                                                                                                                                                                                                      χ,
Υ.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for late
                                                                                                                                                                                                                      McCl
                                                                                                                                                                                                                                                                                                         CS
```

```
A;Introns: 13/2; 106/3; 131/3; 169/2; 241/1 C;Superfamily: triose-phosphate isomerase C;Keywords: gluconeogenesis; glycolysis; homodimer; E;2-249/Product: triose-phosphate isomerase #status F;94,166/Active site: His, Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N; Alternate names: triosephosphate mutase
C:Species: Emericella nidulans, Aspergillus nidulans
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #C:Accession: A25502
R:MCKnight, G.L.; O'Hara, P.J.; Parker, M.L.
Cell 46, 143-147, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-238 <KUR>
A; Cross-references: GB: AE007870; I
C; Genetics:
A; Gene: AGR_L_2166
A; Map position: linear chromosome
                                           δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:D10019; GB:M13362; NID:g217920; PIDN:BAA00908.1; PID:g21792: C:Comment: This enzyme catalyzes the interconversion of glyceraldehyde 3-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-249 <MCK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Nucleotide sequence of the triosephosphate A;Reference number: A25502; MUID:86245050 A;Accession: A25502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
ISASTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
""" Phas 9; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C:Species: Agrobacterium tumefaciens
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
C:Date: 28-0ct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
C:Date: 20-0ct-2001 #sequence_revision 20-0ct-2001 #sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             triose-phosphate isomerase (EC 5.3.1.1) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thiamin-phosphate pyrophosphorylase (AF180145) [imported] - C:Species: Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: thir
A; Map position
                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 47.1
Best Local Similarity 75.1
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 GNAEALAEAVEN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             position: linear chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94 GNAEALAEAVEN 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GNAEHVASAVEN 12
                                        1 GNAEHVASAVENANRVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GNAEHVASAVEN 12
                                                                                                           Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GB:AE007870; PIDN:AAK89656.1; PID:g15159556; GSPDB:GN00170
                                                                                                                                         47.8%;
47.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.8%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47.8%;
75.0%;
                                                                                                           2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               بر
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 43;
Pred. No.
                                                                                                                                      Score 43; DB Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 43;
Pred. No.
                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Emericella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
16;
                                                                                                                                                                    DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ?;
                                                                                                        7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2
                                                                                                                                                                    Length 249
                                                                                                                                                                                                                                                                                                                                  intramolecular oxidoreductase;
                                                                                                                                                                                                                                                                                             predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nidulans
                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-Jun-2000
                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from Aspergillus nid
                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PID:g217921
                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                  isom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŝ
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-461 <KUR>
                                                                                       R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; G
Nucletc Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory
A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: B90555
                                                                                                                                                                                                                                                                                                                                                                                               RESULT
B90555
                                                                                                                                                                                                                                                                                   C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δÃ
                                                                                                                                                                                                                                                                                                                                                       ABC transporter xylose-binding lipoprotein [imported] -
                                                                                                                                                                                                                                                            Accession:
```

в90555

Mycopiasma

pulmonis

(strain

Galisson, F.; Moszer, pathogen Mycoplasma

ס

```
pacB protein - phage P1
C;Species: phage P1
C;Species: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change C;Accession: S21780
C:Accession: S21780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Li, H.; Hodge, D.R.; Pei, G.K.; Seth, A. Gene 143, 303-304, 1994
A;Title: Isolation and sequence analysis of A;Reference number: 138517; MUID:94266173
A;Accession: 138517
                                                                                                                                                                                                                                                                         R;Skorupski, K.; Pierce, J.C.; Sauer, B.; Sternberg, N.
J. Mol. Biol. 223, 977-989, 1992
A;Title: Bacteriophage Pl genes involved in the recogni
A;Reference number: S21779; MUID:92167273
A;Accession: S21780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-297 <RES-
A;Cross-references: EMBL:U07158; NID:g463906; PIDN:AAA20967.1; PID:g463907
C;Superfamily: syntaxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               syntaxin - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998
                                                                                                                                                                                                                           A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-397 <SKO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                       C; Keywords:
                                                                                                                                                                       A; Start codon: GTG
                                                                                                                                                                                          C; Genetics:
                                                                                                                                                                                                         A;Cross-references: EMBL:M74046; NID:g215634; PIDN:AAA21723.1; PID:g215635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          I38517
                                                                Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       257
 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 GNAESTTSIIKNLNSAN 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 EHVASAVENANRVNK 18
                                6 VASAVENANRVNK
VSAAVENAKRONK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EHVKTALENQKKVRK 271
                                                                                                                                                       DNA binding
                                                                   Similarity 9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138517
                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
105
                                 18
                                                                                 47.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47.8%;
53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 43;
Pred. No.
                                                                                   Score 43; DB Pred. No. 30;
                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                              the recognition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the human
                                                                                                   2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 297
                                                                                                Length 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 syntaxin-encoding
                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                            and
                                                                                                                                                                                                                                                                                                            cleavage of the phage
                                                                                                                                                                                                                                                                                                                                                                                  08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-Sep-1999
                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ç
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
```

```
망
                                 δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                  nicotine dehydrogenase (EC 1.5.99.4) chain C - Arthrobacter nicotinovorans C; Species: Arthrobacter nicotinovorans C; Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 21-Jul-2000 C; Accession: I39627; S37570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
C97775
                                                                                                                                                               C;Superfamily: carbon-monoxide dehydrogenase large chain C;Keywords: molybdenum; molybdopterin; oxidoreductase F;226;743/Binding site: molybdopterin cytosine dinucleotide
                                                                                                                                                                                                                                                                                                                                     R;Grether Beck, S.; Igloi, G.L.; Pust, S.; Schilz, E.; Decker, K.; Brandsch, R.
Mol. Microbiol. 13, 929-936, 1994
A;Title: Structural analysis and molybdenum-dependent expression of the pAO1-encoded nid
A;Reference number: 139625; MUID:95115562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Science 293, 2093-2098, 2001
Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acylamino-acid-releasing enzyme [imported] - Rickettsia conorii (strain Malish C;Species: Rickettsia conorii C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AL445566; PID:g14089760; PIDN:CAC13519.1; GSPDB:GN00153
A;Experimental source: strain UAB CTIP
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: MYPU_3460
A;Genetic code: SGC3
                                                                                                                                                                                                                                                           A; Cross-references: EMBL: X75338; NID: g665598; PIDN: CAA53088.1;
                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-814 <GRE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-676 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession:
                                                                                                                                                                                                                             A;Gene: ndhC
                                                                                                                                                                                                                                               C; Genetics:
                                                                                                                                                                                                                                                                                                                        A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE006914; PIDN:AAL03141.1; PID:g15619687; GSPDB:GN00173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: C97775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local (
                                                                                            Query Match
Best Local
                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1: ||: ||: |||
441 GDLEHLKSIVQKANR 455
184 NAEHVVSALYHPGRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       639 GRAEHIGDDLKNANLI 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 8; Consert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GNAEHVASAVENANRV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GNAEHVASAVENANR 15
               2 NAEHVASAVENANRV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RC0603
                                                                          Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                        I39627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
198
                                                                                          47.8%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47.8%;
53.3%;
                                                                      2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.
                                                                      Score 43; DB 1; Pred. No. 64; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 43; DB Pred. No. 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 43; DB
Pred. No. 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2;
                                                                      4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.
                                                                                                           Length 814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                  (Gln,
                                                                                                                                                                                                                                                               PID: g406609
                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                  Glu) #status predicted
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R
```

Search completed: June 10, Job time: 204 sec

2002, 15:22:24

```
Rifleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995

A; Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente A; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A; Reference number: A64000; MUID:95350630

A; Accession: F64018
A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                  A;Residues: 1-163 <TIGR>
A;Cross-references: GB:U32784; GB:L42023; NID:g3212210; PIDN:AAC22694.1; C;Superfamily: hypothetical protein b0426
В
                                           Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
F64018
                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change
C;Accession: F64018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        conserved hypothetical protein HII034 - Haemophilus influenzae (strain Rd KW20) C_i; Species: Haemophilus influenzae
                                                                                           Query Match
Best Local Similarity
Matches 9; Conserv
15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15
                                                σ
VRNAVENANRV
                                             VASAVENANRV 16
                                                                                                Conservative
25
                                                                                                                    46.7%;
                                                                                                ۲.
                                                                                                                    Score 42;
Pred. No.
                                                                                                Mismatches
                                                                                                                       16;
                                                                                                                                              2
                                                                                                                                        Length 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-Jul-2000
                                                                                           0;
                                                                                             Gaps
                                                                                                                                                                                                                                         PID:g1574067
                                                                                             0
```

```
먕
                         δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1
AAB35466
                                                                                        뫄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q
                                           Query Match
Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                 protein. Note: The present sequence is stated as being the columns 7-10 in the specification (see AAB35471). differ at three positions.
                                                                                                                                                  The present invention describes a method of diagnosing infection by enterohaemorrhagic Escherichia coli 0157:H7 by contacting a body fl sample with EspA or EspB and detecting the presence of antibodies coli infection causes haemorrhagic colitis and can lead to death or
                                                                                                                                                                                                                                                                                                                 21-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                   20-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                     US6204004-B1
                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli EspB #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB35466 standard;
                                                                                        Sequence
                                                                                                                                                                                              Disclosure; Column 17-20; 19pp; English.
                                                                                                                                                                                                                           comprises
                                                                                                                                                                                                                                    Diagnosis
                                                                                                                                                                                                                                                                               Kaper JB,
                                                                                                                                                                                                                                                                                                                                  21-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB35466;
                                                                                                                                                                                                                                                                                                (UYMA-)
                                                                                                                                             term liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                366
          197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11
                           w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ب
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNAEHVASAVENANRVN 17
                           AEHVASAVENANRVNK 18
                                                                                                                                                                                                                                                            2001-256675/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glfqnlanqvqnanrln 382
                                                                                                                                         infection causes haemorrha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            food
                                                                                                                                                                                                                                                                                                VIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
8; Conserv
                                            Similarity
8; Conser
                                                                                                                                                                                                                                                     AAF58936
                                                                                                                                                                                                                        of active infection by enterohemorrhagic detecting antibodies to E. coli secreted
                                                                                                                                                                                                                                                                              Jarvis K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           poisoning; haemorrhagic colitis;
                                                                                       312 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                 97US-0821872
                                                                                                                                                                                                                                                                                                                                 97US-0821872
                                                                                                                                                                                                                                                                                                                                                                                             /note=
219
                                                                                                                                                                                                                                                                                                                                                                                                                                 199
                                                                                                                                                                                                                                                                                                                                                                                                                203
                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                      /note=
                                                                                                                                                                                                                                                                                                                                                                                                                       'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.8%;
47.1%;
                                                     46.7%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                     "encoded by
                                                                                                                                                                                                                                                                                                                                                                                                     "encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                       "encoded by AAT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  312 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 43; DB Pred. No. 1.2e. 6; Mismatches
                                                    Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6,
                                         Pred. No. 82;
3; Mismatches
                                                                                                                                           sequence is
                                                                                                                                                                                                                                                                                                                                                                                     AAA"
                                                                                                                                                                                                                                                                                                                                                                                                     CCC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; DB 22;
. 1.2e+02;
                                                     DB
82;
                                                            22;
                                                                                                                                           one version of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E. coli 0157:H7
                                          5
                                                            Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 605
                                                                                                               same as that given in However, the sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                           Indels
                                                                                                                                                                                                                         Escherichia coli
protein EspA or
                                                                                                                                           the EspB
                                                                                                                                                                                                                         EspA or EspB
                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                    by
fluid
                                                                                                                                                    long
                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
WXX DXXX XXX
```

```
AAU34
                                                                                                                                      Ъ
                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
                                                                                                                                                                                     Query Match
Best Local S
Matches 7
 E. coli cellular proliferation
                         14-FEB-2002
                                                  AAU34565;
                                                                           AAU34565 standard; Protein;
                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                         specification, but was obtained in electronic
at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                      The sequence data for this patent did not form specification, but was obtained in electronic :
                                                                                                                                                                                                                                                                                                                                     cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 18954; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid genes from Drosophila and interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB64054 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB64054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PEKE ) PE CORP NY
                                                                                                                                      240 nsqhiatalekatav
                                                                                                                                                                                                                                                                                                                 ABB57737-ABB72072
                                                                                                   13
                                                                                                                                                              2 NAEHVASAVENANRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-656860/75
DB; ABL08157.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JC,
                                                                                                                                                                                      Similarity 46.7; Conservative
                                                                                                                                                                                                                                                                                                                            (ABL01840-ABL16175) and
                                                                                                                                                                                                                                                   378 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-191637P
2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001WO-US09231
                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                               16
                                                                                                                                                                                                  46.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ŀ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , DWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                             detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                           481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            378
                                                                                                                                                                                       5
                                                                                                                                                                                     Score 42; DB 22; Pred. No. 1e+02; 5; Mismatches
protein #146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Myers
                                                                           Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ã
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 18954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EW;
                                                                                                                                                                                                                                                                                                                            encoded
                                                                                                                                                                                                                                                                                      n part of the printed format directly from
                                                                                                                                                                                                            Length 378;
                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                      invention
                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                       WIPO
                                                                                                                                                                                                                                                                                                                                                                           and
                                                                                                                                                                                                                                                                                                                                                                                      is
                                                                                                                                                                                     0;
```

δÃ

Antisense; prokaryotic cellular proliferation protein;

```
RESULT
AAR4388
ID AA
XX
AC AA
XX
DT 25
XX
DE C-
XX
                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                 The invention relates to antisense inhibitors of genes essential to CC prokaryotic cellular proliferation, their use in identifying the CC genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faccalis. The CC invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, CC and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in essential prokaryotic cellular proliferation protein.

Note: The sequence data for this pattent did not form part of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                         Matches
                                                                                                                3880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-MAR-2000;
23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
              C-terminal portion of BCV spike
                                          25-MAY-1994
                                                                     AAR43880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haselbeck R,
Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200170955-A2
                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibiotics, comprise sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibiotic;
                                                                                              AAR43880 standard; protein; 179 AA
                                                                                                                                                                                                                                                                                                                                       of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ELIT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-NOV-2000;
22-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli.
                                                                                                                                                                    39
                                                                                                                                                                                                                                      Local
                                                                                                                                                                                             2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polynucleotides for the identification and development lbiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-611495/70.
DB; AAS52424.
                                                                                                                                                                                             NAEHVASAVENA 13
                                                                                                                                                                   saehlasalesa
                                                                                                                                                                                                                       8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                       .int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq ID No 10158; 511pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-206848P.
2000US-207727P.
2000US-242578P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibacterial;
                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001US-269308P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-253625P.
2000US-257931P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001WO-US09180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-191078P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ohlsen
Xu HH;
                                                                                                                                                                   50
                                                                                                                                                                                                                                    46.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zyskind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    drug design.
                                                                                                                                                                                                                                   Score 42; DB 22;
Pred. No. 1.3e+02;
              protein (Strain Bcve2).
                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ä,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wall D,
                                                                                                                                                                                                                                                 Length 481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trawick JD,
                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Of
                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carr
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ښ;
                                                                                                                                                                                                                      0,
```

```
밁
                                                                                                                                                                                                                                                                                                                                                   δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR43883
                                                                                                                                                                                                                                                                                             RESULT 15
                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                The polypeptide comprises a sequence which is highly conserved among coronaviruses and which is capable of eliciting an immune response. The polypeptide and nucleic acid can be used to produce vaccines which can be used to protect animals against different members of the coronavirus family. e.g. feline infectious peritonitis virus, feline enteric coronavirus; canine coronavirus, swine transmissable gastroenteritis coronavirus; bovine coronavirus; human coronavirus
                                                                                                                                                                Coronavirus; spike protein; S protein; vaccine; FIPV; mouse hepatitis virus.
                                                                                                                                                                                                   C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a conserved domain of coronavirus encoding it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Universal corona-virus vaccine - comprising a polypeptide contg. a conserved domain of coronavirus S protein or nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Coronavirus; spike protein; S protein; vaccine; bovine coronavirus.
                              (SMIK ) SMITHKLINE BEECHAM CORP.
                                                     08-MAY-1992;
                                                                          07-MAY-1993;
                                                                                               25-NOV-1993
                                                                                                                     WO9323421-A
                                                                                                                                         Mouse hepatitis virus
                                                                                                                                                                                                                          25-MAY-1994
                                                                                                                                                                                                                                                AAR43883;
                                                                                                                                                                                                                                                                     AAR43883 standard; protein; 180
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                       or avian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1993-386472/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09323421-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bovine coronavirus
                                                                                                                                                                                                                                                                                                                              111 gngnhiislvqna
                                                                                                                                                                                                                                                                                                                                          1 GNAEHVASAVENA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E۷
                                                                                                                                                                                                                                                                                                                                                                          Similarity 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                       infectious bronchitis virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                  179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Klepfer S,
                                                                                                                                                                                                  portion of MHV
                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-25; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                  A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92US-0882171
                                                     92US-0882171.
                                                                          93WO-US04365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93WO-US04365
                                                                                                                                                                                                                                                                                                                                                    13
                                                                                                                                                                                                                                                                                                                                                                                    45.6%;
53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Miller TJ,
                                                                                                                                                                                                 spike protein (Strain Mhve2a59).
                                                                                                                                                                                                                                                                                                                                                                          Score 41; DB Pred. No. 64; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reed
                                                                                                                                                                                                                                                                                                                                                                                     DB
64;
                                                                                                                                                                                                                                                                                                                                                                                                14;
                                                                                                                                                                                                                                                                                                                                                                           4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BCV;
                                                                                                                                                                                                                                                                                                                                                                                                Length 179;
                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                          Gaps
```

Jones EV,

Klepfer S,

Miller TJ,

Reed

8888888x&

밁 Š

```
RESULT AAYOTO78
ID AAYO XX AAYO AC AAYO AC AAYO XX Canc KW breas XX Canc KW breas XX Canc FN WO99 AX CAC FN 15-J XX CAC FN 10-C FN 11-C FN 11-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SXX XXX PTT PTT •
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 8
  The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the
                                                                                                                                                   Disclosure;
                                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                                                           Pireundschuh
                                                                                                                                                                                                                                                                                                                                                                 Chen Y,
                                                                                                                                                                                                                                                                                                                                                                                                          (LUDW-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-OCT-1997
10-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09904265-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cancer associated and breast cancer; colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Renal cancer associated antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY07078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY07078 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence is used fo Aspergillus through the integration into the chr 16 and AAP70497-98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 1; 79pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New recombinant plasmids to integrate in Aspergillus chromosomal DNA - useful for expressing higher eucaryotic genes esp. when plasmid contains transcriptional promoter, eg DNA encoding alcohol dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-JUL-1997
                                                                                                                                                                                                                  isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GNAEHVASAVENANRVN 17
                                                                                                                                                                                                     isolated cancer associated nucleic acids and polypeptides lated using sera from cancer patients, used to develop produced using sera from cancer patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                            1999-132448/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gnaesttsiiknlnsan
                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                        diagnosis, monitoring
                                                                                                                                                                                                                                                                                                                                                                                                          LUDWIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                 Gout
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       250 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                           ĭ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                               Ļ
                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0061599.
97US-0061765.
97US-0948705.
97GB-0021697.
                                                                                                                                                                                                                                                                                                                                                                                                        INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0102322
97US-0896164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-US14679
                                                                                                                                                   484;
                                                                                                                                                                                                                                                                                                                                         Gure
Sahin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47.88;
47.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the use of a recombinant plasmid chromosome DNA of Aspergillus.
                                                                                                                                               787pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for
                                                                                                                                                                                                                                                                                                                                           Ċ, Þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or expressing higher eucaryotic genes in use of a recombinant plasmid capable of romosome DNA of Aspergillus. See also AAN70814-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English
                                                                                                                                                                                                                                                                                                                                         O'Hare M,
Scanlan MG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2
                                                                                                                                               English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gastric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
Pred.
                                                                                                                                                                                          or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             precursor sequence
                                                                                                                                                                                          treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No.
                                                                                                                                                                                                                                                                                                                                         Ĭ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer;
                                                                                                                                                                                                                                                                                                                                       Obata Y, (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        research;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
44;
                                                                                                                                                                                          of cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
(d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch; treatment;
renal cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
                                                                                                                                                                                                                                                                                                                                       old
t E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                           []
                                                                                                                                                                                                         products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
```

The sequence data specification, but at ftp.wipo.int/pu

scirication, but was obtained in electronic ftp.wipo.int/pub/published_pct_sequences.

for this patent did not form

format directly

part

of the

printed

from

WIPO

Sequence

605

```
ABB67887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
insecticides, therapeutics and pharmaceutical drugs. The Invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                  The invention relates to an isolated nucleic acid detection reagencepable of detecting 1000 or more genes from Drosophila. The inventueful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigens. The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast
                                                                                                                                                                 Disclosure;
                                                                                                                                                                                                                                                                             N-PSDB; ABL11990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                     genes from Drosophila
interactions -
                                                                                                                                                                                                                                        New isolated nucleic
                                                                                                                                                                                                                                                                                                                                                                                                      23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster polypeptide
                                                                                                                                                                                                                                                                                                                                 Venter
                                                                                                                                                                                                                                                                                                                                                                   (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB67887;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB67887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
                                                                                                                                                                                                                                                                                              2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ehvktalengkkvrk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EHVASAVENANRVNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer
                                                                                                                                                                                                                                                                                                                                JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    renal cancer, colon cancer, gastric cancer, prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  297
                                                                                                                                                                 SEQ ID
                                                                                                                                                                                                                                                                                                                                Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   developmental biology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    2000US-191637P
2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                     e acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18
                                                                                                                                                                 30453;
                                                                                                                                                                                                                                                                                                                                Ŀ
                                                                                                                                                                                                                                                                                                                                PWD,
                                                                                                                                                                                                                  detection reagent for detecting for elucidating cell signalling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 43; DB Pred. No. 54; 3; Mismatches
                                                                                                                                                              21pp
                                                                                                                                                                                                                                                                                                                                Myers
                                                                                                                                                                 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ
                                                                                                                                                              Sequence Listing;
                                                                                                                                                                                                                                                                                                                                EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ħ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                              English
                                                                                                          The invention
                                                                                                                                                                                                                    1000
and c
                                                                                                                              reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                    0 or more cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                         and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and
                                                                                                          is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
```

```
RESULT
AAM52135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                           δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence comprises the minimal P1 pac site. It was used in the construction of the pathogen and tissue-specific toxic agents of the invention. These agents may be antisense sequences, ribozymes or toxic proteins. These can be used in the treatment of cancer and infections including hepatitis, herpes, malaria, bacterial meningitis, typhoid fever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New recombinant nucleic acid comprising a nucleotide sequence encoding one or more toxic agents operably linked to a pathogen specific or tissue specific promoter is useful for inhibiting replication of a
                                                                                                                                                                                                                      Infection; antisense RNA; ribozyme; DNAzyme; antiviral; gene therapy; papilloma virus; hepatitis B virus; cytotoxic; cytostatic; wart; cervical dysplasia; cervical carcinoma; carcinoma; laryngeal papillom
                                                                                                                                                           Misc-difference
                                                                                                                                                                                          Bacteriophage p1
                                                                                                                                                                                                                                                                    Minimal P1
                                                                                                                                                                                                                                                                                         05-FEB-2002
                                                                                                                                                                                                                                                                                                                                  AAM52135 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 12; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Norris J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MUSC-) MUSC FOUND RES DEV. (UYPE-) UNIV PENN STATE.
Norris JS,
                    (UYSC-) UNIV SOUTH CAROLINA (PENN-) PENN STATE RES FOUN
                                                   13-APR-2000;
07-DEC-2000;
                                                                                                                            WO200179524-A2
                                                                                                                                                                                                                bacteriophage
                                                                                                                                                                                                                                                                                                               AAM52135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-APR-1999;
13-APR-2000;
                                                                                  13-APR-2001; 2001WO-US12130
                                                                                                                                                                                                                                                                                                                                                                                        \omega_{\omega}
                                                                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                                                                                                                                                                                                         7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                            VASAVENANRVNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000-638570/61
                                                                                                                                                                                                                                                                                                                                                                                     vsaavenakrqnk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'n

    Similarity
    Conserv

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clawson G,
                                                                                                                                                                                                                                                                    pac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 AA;
Clawson GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0291902
2000US-0548449
                                                   2000US-0548449
2000US-251810P
                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                P1;
                                                                                                                                                                                                                                                                    site
                                                                                                                                                          Location/Qualifiers
                                                                                                                                                 /note=
                                                                                                                                                                                                               pac site
                                                                                                                                                                                                                                                                                                                                                                                                           18
                                                                                                                                                                                                                                                                                                                                   Protein;
                                                                                                                                                                                                                                                                                                                                                                                        45
                                                                                                                                                                                                                                                                   sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                          47.8%;
69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Westwater
                                                                                                                                                "Encoded by CAA"
                     FOUND
Westwater
                                                                                                                                                                                                                                                                                                                                   59
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 43;
Pred. No.
                                                                                                                                                                                                                                                                   protein.
                                                                                                                                                                                                                                                                                                                                   A
                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ņ
c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schofield D,
                                                                                                                                                                                                                                                                                                                                                                                                                                           00
Schofield
                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
8.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     21;
                                                                                                                                                                                                                                                                                                                                                                                                                                2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 59
'n
                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                      laryngeal papilloma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schmidt M,
Schmidt MG;
                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hoel
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ₩,
                                                                                                                                                                                                                                                                                                                                                                                                                                0;
```

```
RESULT
AAP70496
                                               PR
PX
PX
PI
                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ΧX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             delivery of one or more toxic gene products, antisense RNAs, ribozymes, DNAzymes or a combination thereof. The nucleic acids have antiviral activity and can be used in gene therapy. They are useful for the treatment of papilloma or hepatitis virus induced conditions and can produce a cytotoxic or cytostatic effect in papillomavirus or hepatitis infected cells. The papilloma virus induced condition is selected from warts, cervical dysplasia, cervical carcinoma, carcinoma in situ and
WPI; 1987-221265/31.
N-PSDB; AAN70813.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          associated with the transformation or plasmid copy number control, hybridises to a viral polyadenylation signal or a core, pre core o polymerase encoding sequence. Specifically, the invention relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            order to treat and/or eradicate the infection. In particular tinvention relates to at least one nucleic acid molecule, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          characterisation of toxic agents lethal to pathogens and methoderise such toxic agents to a pathogen or pathogen infected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acid for the treatment of papilloma or hepatitis virus induced conditions comprises a catalytic region which produces a cytotoxic or cytostatic effect in the infected cell -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-607700/69
N-PSDB; ABA02577.
                                            McKnight GL,
                                                                                                        13-JAN-1987;
17-JAN-1986;
                                                                                                                                                                                                                      W08704464-A
                                                                                                                                                                                                                                                    Aspergillus
                                                                                                                                                                                                                                                                                   tpiA'gene;
                                                                                                                                                                                                                                                                                                                                                 27-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                AAP70496
                                                                                                                                                                                                                                                                                                                                                                                                               AAP70496 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     silent mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          laryngeal papilloma. The present sequence is that of a modified bacteriophage P1 pac site sequence rendered defective due to several
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            specifically hybridises to mRNA encoding at least one vital protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to the discovery,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Examples; Fig 12; 143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hoel B,
                                                                           (ZYMO-) ZYMOGENETICS INC
                                                                                                                                                        15-JAN-1987;
                                                                                                                                                                                       30-JUL-1987
                                                                                                                                                                                                                                                                                                                Aspergillus nidulans tpiA genomic clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity hes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 vsaavenakrqnk 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 VASAVENANRVNK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dolan J,
                                                                                                                                                                                                                                                                                   triose-phosphate-isomerase; enzyme; promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                (first entry)
                                            Upshall A;
                                                                                                        87US-0946873
86US-0820519
                                                                                                                                                        87WO-US00119
                                                                                                                                                                                                                                                                                                                                                                                                              protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                               250 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
8.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            methods for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              relates to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ٥ŗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'n
```

```
RESULT
AAR13991
ID AAR1
                                                                                                                  20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
AAR13992
                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                 Query Match
Best Local
AAR13991 standard; Protein;
                                                                                                                                              Vector pDS56/RBSII, 6xHis is a derivative of pDS56/RBS (EP-282042). It comprises an additional sequence encoding six histidine residues. Into this vector may be ligated a 1400 bp AseI fragment of NXY (see AAQ13727) to yield pDS-NXY. E. coli Sc13009 (pUBAI) transformed with pDS-NXY produces a 69 kD fusion protein comprising the NXY fragment N-terminally linked to an affinity peptide contg. 6 His units, and C-terminally to a vector-derived sequence. Fragment B corresponds to amino acids 1-462 of the N-terminal of the antigen. The affinity peptide is used for the purification of the antigen. The polypeptide is useful for the produced of the antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P. falciparum sporozoite antigen
                                                                                                                                         purification of the antigen. The production of antimalarial vaccines
                                                                                                                                                                                                                                        Claim 2; Page 18; 36pp; German.
                                                                                                                                                                                                                                                         New antimalarial polypeptide(s) - corresp. to specific epitope(s) of the Plasmodium falciparum sporozoite antigen, and are useful as vaccines or to prepare antigens
                                                                                                                                                                                                                                                                                                          Certa U,
                                                                                                                                                                                                                                                                                                                                                                                            EP447956-A.
                                                                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-DEC-1991
                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                           23-MAR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR13992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR13992 standard; Protein;
                                                                                                                                  See also
                                                                                                                                                                                                                                                                                         WPI; 1991-282989/39
                                                                                                                                                                                                                                                                                                                          (HOFF ) HOFFMANN-LA ROCHE AG
                                                                                                                                                                                                                                                                                                                                                           14-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                           25-SEP-1991
                                          26
                                                          N
                   տ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4
                                                         NAEHVASAVENANRVNK 18
                                          navhkinavdkvnavnk
                                                                         Similarity 52.9
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YXN
                                                                                                                                  AAQ13727-8
                                                                                                                                                                                                                                                                                                         Guttinger
                                                                                                                  493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene; malaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                  A
                                                                                                                                                                                                                                                       to prepare antigens
                                                                                                                                                                                                                                                                                                                                          90CH-0000970
                                                                                                                                                                                                                                                                                                                                                           91EP-0103920
                                                                                                                                                                                                                                                                                                                                                                                                                            484..493
                                                                                                                                                                                                                                                                                                                                                                                                          /note= "vector-encoded_peptide'
                                                                                                                                                                                                                                                                                                                                                                                                                                                          note- "affinity peptide including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                   'label=
                                                                                                                                                                                                                                                                                                                                                                                                                                   note- "amino
                                                                                                                                                                                                                                                                                                                                                                                                                                           'label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label=
                                                                                                                                                                                                                                                                                                          ž
                                                                                 48.9%;
                                                                                                                                                                                                                                                                                                          Matile
  713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     493
                                                                        Score 44; DB Pred. No. 66; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibodies;
                                                                         ?
                                                                                                                                                                                                                                                                                                                                                                                                                                   acids 1-462 of the
                                                                                                                                                                                                                                                                                                          Η;
  A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fusion
                                                                               DB
66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   purification; affinity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptide.
                                                                                        12;
                                                                        6
                                                                                        Length 493;
                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide in
                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                                                                                                                                                                           His
                                                                                                                                                                                                                                                                                                                                                                                                                                                          residues"
                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR13991"
                                                                        Gaps
                                                                        0;
                                                                                                                                                AAB27206
ID AAB2
                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                      Qγ
                                                                                                                                                                 RESULT
                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                Query Match
Best Local
                                                                       Bacteria;
bacterial
14-APR-2000; 2000WO-US10229
                19-OCT-2000
                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                          Certa U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR13991;
                                                                                                                                AAB27206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vaccine;
                                                                toxic
                                                                                                                                                                                         Ŋ
                                                                                                                                                                                                        N
                                                                                                                                                               σ
```

```
rulypeptides corresp. in at least one specific epitope with the P. falciparum sporozoite are useful in the prodn. of antimalarial vaccines. The N-terminal has a mol.wt. of 81.281, the total protein has a mol.wt. above 200 kD. Potential glycosylation sites are at position 32, 260, 308, 323, 329, 344, 362, 365, 377, 380, 387, 388, 394, 398, 399, 406, 414, 537, 554, 659, 684, 693, 702, and 705. See also AAQ13728.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antimalarial polypeptide(s) - corresp. to specific epitope(s) of the Plasmodium falciparum sporozoite antigen, and are useful as vaccines or to prepare antigens
                                    Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 16; 36pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP447956-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium falciparum sporozoite antigen N-terminal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-DEC-1991
WO200061804-A1
                                                                                                                                            Bacteriophage delivery plasmid minimal P1
                                                                                                                                                                                 27-FEB-2001
                                                                                                                                                                                                                                                        AAB27206 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAQ13727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HOFF ) HOFFMANN-LA ROCHE AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 52.9 hes 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                        NAEHVASAVENANRVNK 18
                                                                                                                                                                                                                                                                                                                                                   navhkinavdkvnavnk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1991-282989/39.
                                                                     protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YXN
                                                                                    infection; drug-resistant pathogen;
meningitis; tuberculosis; antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Guttinger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 713 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90CH-0000970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91EP-0103920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      malaria; antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Z
                                                                                                                                                                                                                                                                                                                                                                                                                                              52
52
                                                                                                                                                                                                                                                                                                                                                     21
                                                                                                                                                                                                                                                                                                                                                                                                                                            . 9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matile
                                                                                                                                                                                                                                                          59
                                                                                                                                                                                                                                                                                                                                                                                                                         2;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
Pred.
                                                                                                                                                                                                                                                          B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                            44;
                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 12;
1e+02;
                                                                                                                                            pac
                                                                                      cancer; typhoid fever;
strand; ribozyme;
                                                                                                                                            site peptide
                                                                                                                                                                                                                                                                                                                                                                                                                         6
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 713;
                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         0;
```

밁 Qy

100.0%;

0,

```
RESULT
AAY33651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 x 0 0 0 0 0 0 0 x 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes a novel protein which has hemolytic activity, blood platelet agglutination activity and a molecular weight of about 50,000 Da (by SDS-PAGE). The protein, homologs and analogs of the invention can be used as a novel approach to developing drugs useful for the treatment of jelly fish stings, pharmaceuticals with blood platelet agglutination activity, pesticides by use of the hemolytic activity, and in the study of the hemolytic mechanism. AAY33648-Y33650 represent fragments of the hemolytic protein described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY33651;
                                      This invention describes a novel protein which has hemolytic activity, blood platelet agglutination activity and a molecular weight of about 50,000 Da (by SDS-PAGE). The protein, homologs and analogs of the invention can be used as a novel approach to developing drugs useful for the treatment of jelly fish stings, pharmaceuticals with blood platelet agglutination activity, pesticides by use of the hemolytic activity, and in the study of the hemolytic mechanism. This sequence represents the
                                                                                                                                                                                                                                                                                                                                                                                                                                     07-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C. rastonii hemolytic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY33651 standard;
                                                                                                                                                              Claim
                                                                                                                                                                                                     Protein with hemolytic activity, useful for drugs treating jelly fish stings, pharmaceuticals with blood platelet agglutination activity, pesticides by use of the hemolytic activity, and study of the hemolytic
                                                                                                                                                                                                                                                                                                                Nagai H,
                                                                                                                                                                                                                                                                                                                                                                          01-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                      30-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9950294-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carybdea rastonii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hemolytic protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                           (SUNR ) SUNTORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ۳
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GNAEHVASAVENANRVNK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N
                                                                                                                                                                                                                                                                   1999-580740/49
DB; AAZ23610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gnaehvasavenanrvnk 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
                                                                                                                                                             4; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                              Nakajima T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 22-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sting;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first
                                                                                                                                                             26-27;
                                                                                                                                                                                                                                                                                                                                                                          98JP-0088569
                                                                                                                                                                                                                                                                                                                                                                                                      99WO-JP01607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; blood platelet agglutination; drug development; jellyfish; pharmaceutical; pesticide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32pp; Japanese
                                                                                                                                                             32pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 90;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 20,
6.9e-08;
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
```

0,

Query Match

100.0%;

Score

90;

DB 20;

Length 450;

밁 Š

0

Sequence

ÃĂ,

nemolytic

protein 450

described in the invention

```
RESULT
AAW75903
                                                                       Query Match
Best Local S
Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                       Monoclonal antibodies that specifically recognise any of these foam proteins are used in immunoassays (preferably ELISAs) for determining the foam protein content of beer during brewing, for determining the head retention or head retention stability of beer, for evaluating raw materials for beer making, and for selecting stabilisers (preferably silica gel or tannic acid) for beer. The immunoassays allow investigation of raw materials and stability during fermentation rathe than after and they are an improvement on prior art assays involving polyclonal antibodies and allow detection of minute amounts of ingredient-specific foam proteins.
                                                                                                                                                                                                                                                                                                                                                                                                          Sequences shown in AAW75903 to AAW75908 are novel foam proteins with molecular weight between 40-48 kD, as determined by Western blot analysis. These foam proteins are crucial for beer head retention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-DEC-1997;
07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
Hordeum sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Foam protein; beer head retention; ELISA; brewing; beer stability; be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW75903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW75903 standard; peptide;
                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Page 5; 17pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        stabiliser for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New foam proteins crucial for head retention of beer
by monoclonal antibodies used in immunoassays to assay
content, head retention and raw materials of beer and t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-458799/40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP863153-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel foam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SUNR ) SUNTORY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tannic acid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ishibashi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 
les 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GNAEHVASAVENANRVNK
سو
                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ω
                AVENANRVNK
avenanrvnk 10
                                                                                                                                                                          19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein 1 for beer
                                                                     Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kakui T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fermentation.
                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97JP-0334229
97JP-0053249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98EP-0103922
                                  18
                                                                       54.4%; Score 49; DB
100.0%; Pred. No. 0.
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nakatani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 2.6e-06; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              head
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  on; monoclonal antibody; immunoassay;
beer making; stabiliser; silica gel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ×
`
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 retention of beer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            retention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Terano
                                                                                            DB 19;
0.27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          beer and to select
                                                                                                               Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                           fermentation rather
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           foam protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 recognised
                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                      raw
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ω
```

```
Search completed: June 10, 2002, 15:29:16 Job time: 486 sec
                                                                                                                                                                                                                                                      Query Match 52.8%;
Best Local Similarity 41.7%;
Matches 5; Conservative
                                                                                                                                        1 GEIQTKPDRVGQ 12
| ::||| ::|:
| 1195 GSLETKPKKIGK 1206
                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF02373; jmjC; 1.
Pfam; PF02375; jmjN; 1.
Pfam; PF00096; zf-C2H2; 4.
SMART; SM00355; ZnF_C2H2; 4.
SMART; SM00355; ZnF_C2H2; 4.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
DNA-binding; Metal-binding; Zinc-finger.
SEQUENCE 1360 AA; 152628 MW; A45A5801285EBA16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

EU Arabidopsis sequencing project;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL049659; CAB41155.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Choisne N., Robert C., Brottier P., Wincker P., Cattolico L., Artiguenave F., Saurin W., Weissenbach J., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003347; JmjC.
InterPro; IPR003349; JmjN.
InterPro; IPR000822; Znf-C2H2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                   Score 38; DB 10; Length 1360; Pred. No. 4.5e+02; 5; Mismatches 2; Indels
                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                      0;
```

OCCOCK
OC

Qy 멍

```
Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                 Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq
Maximum DB seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OM protein -
                       55
7
11
11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                 Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           greater t
s derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A_Geneseq_032802:*
1: /SIDS1/gcgdata/hd
2: /SIDS1/gcgdata/hd
3: /SIDS1/gcgdata/hd
                                                                                                                                                                                                                                                                                                                                                                                             Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is the number of results predicted by chance to have ter than or equal to the score of the result being prived by analysis of the total score distribution.
                                                  100.0
100.0
54.4
48.9
48.9
47.8
47.8
47.8
47.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 June 10, 2002, 15:21:06; Search time 73.49 Seconds (without alignments) 27.205 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-647-522-2
90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. ISIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1990.DAT:*

SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1990.DAT:*

SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1990.DAT:*

SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1992.DAT:*

SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1993.DAT:*

SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1993.DAT:*

SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1995.DAT:*

SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1995.DAT:*

SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1995.DAT:*

SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT:*

SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT:*

SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT:*

SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1990.DAT:*

SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT:*

SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  747574 seqs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GNAEHVASAVENANRVNK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1985.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1986.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1987.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1988.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \times \frac{\gamma_{\text{SIDSL}}/\text{gcgdatta/hold-geneseg/genesegp-embl/AA1980_DAT:*}{\text{SIDSL}/\text{gcgdatta/hold-geneseq/genesegp-embl/AA1981_DAT:*}{\text{SIDSL}/\text{gcgdatta/hold-geneseq/genesegp-embl/AA1982_DAT:*}{\text{SIDSL}/\text{gcgdatta/hold-geneseq/genesegp-embl/AA1983_DAT:*}{\text{SIDSL}/\text{gcgdatta/hold-geneseq/genesegp-embl/AA1983_DAT:*}{\text{SIDSL}/\text{gcgdatta/hold-geneseq/geneseqp-embl/AA1984_DAT:*}{\text{SIDSL}/\text{gcgdatta/hold-geneseq/geneseqp-embl/AA1984_DAT:*}{\text{SIDSL}/\text{gcgdatta/hold-geneseq/geneseqp-embl/AA1984_DAT:*}{\text{SIDSL}/\text{gcgdatta/hold-geneseq/geneseqp-embl/AA1984_DAT:*}{\text{SIDSL}/\text{gcgdatta/hold-geneseq/geneseqp-embl/AA1984_DAT:*}{\text{SIDSL}/\text{gcgdatta/hold-geneseq/geneseqp-embl/AA1984_DAT:*}{\text{SIDSL}/\text{gcgdatta/hold-geneseq/geneseqp-embl/AA1984_DAT:*}{\text{SIDSL}/\text{gcgdatta/hold-geneseq/geneseqp-embl/AA1984_DAT:*}{\text{SIDSL}/\text{gcgdatta/hold-geneseq/geneseqp-embl/AA1984_DAT:*}{\text{SIDSL}/\text{gcgdatta/hold-geneseq/geneseqp-embl/AA1984_DAT:*}{\text{SIDSL}/\text{gcgdatta/hold-geneseq/geneseqp-embl/AA1984_DAT:*}{\text{SIDSL}/\text{gcgdatta/hold-geneseq/geneseqp-embl/AA1984_DAT:*}{\text{SIDSL}/\text{gcgdatta/hold-geneseq/geneseqp-embl/AA1984_DAT:*}{\text{SIDSL}/\text{gcgdatta/hold-geneseq/geneseqp-embl/AA1984_DAT:*}{\text{gcgdatta/hold-geneseq/geneseqp-embl/AA1984_DAT:*}{\text{gcgdatta/hold-geneseq/geneseqp-embl/AA1984_DAT:*}{\text{gcgdatta/hold-geneseq/geneseqp-embl/AA1984_DAT:*}{\text{gcgdatta/hold-geneseq/geneseqp-embl/AA1984_DAT:*}{\text{gcgdatta/hold-geneseq/geneseq-embl/AA1984_DAT:*}{\text{gcgdatta/hold-geneseq/geneseq-geneseq-embl/AA1984_DAT:*}{\text{gcgdatta/hold-geneseq/geneseq-geneseq-geneseq-geneseq-embl/AA1984_DAT:*}{\text{gcgdatta/hold-geneseq/geneseq-geneseq-geneseq-geneseq-geneseq-geneseq-geneseq-geneseq-geneseq-geneseq-geneseq-geneseq-geneseq-geneseq-geneseq-geneseq-geneseq-geneseq-geneseq-geneseq-geneseq-geneseq-geneseq-geneseq-geneseq-geneseq-geneseq-geneseq-geneseq-geneseq-geneseq-geneseq-geneseq-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.
                                                                                                                                                                                                                                                                                                                                                                                             Length
                    18
450
493
493
713
713
723
70
59
250
250
257
                                                                                                                                                                                                                                                                                                                                                                                                 ВВ
             20
22
22
                                                                                                              20
20
19
12
12
12
21
8
          AAX33649
AAX753651
AAX753651
AAX75961
AAX13992
AAX13991
AAX27206
AAX27206
AAX52135
AAX970496
AAX970496
AAX970496
AAX970496
AAX970496
                                                                                                                                                                                                                                                                                                                                                                                             ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
Bacteriophage deli
Minimal Pl pac sit
Aspergillus nidula
Renal cancer assoc
Drosophila melanog
Escherichia coli E
                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                                                                                                         C. rastonii hemoly
                                                                                                                                                                                           P. falciparum spor
Plasmodium falcipa
                                                                                                                                                                                                                                                              Novel
                                                                                                                                                                                                                                                              toam protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               printed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
AAY33649
```

			•
	4446660 0000000000000000000000000000000	44444444	4444444422
\$ 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	4444000		45.66.7 45.66.7 45.66.6
312 312 380 478 583 975	1159 1159 1164 1164 1167 1367 218 229 229 245	72 297 476 576 583 711 788 921 1109	378 481 1179 180 180 590 590 1363
22 22 23 21 22 22	118 118 120 220 220	16 22 21 21 21 21 22 22 22 22 22 22	22 22 114 114 21 121 121
AAX19936 AAB35471 AAR21850 AAB56914 AAU35615 AAR07999 ABB61030	.AAW40371 AAW01570 AAW01575 AAW01571 AAW01571 AAY84035 AAW25257 AAY19937 AAY19937	AAR/1349 ABB63579 AAB23646 AAG46178 AAG46177 AAG46176 AAG46176 AAG46176 ABB68264 ABB68264 ABG09633 ABG20529 AAY84034	ABB64054 AAU34565 AAR43880 AAR43883 AAAR43883 AAAR43884 AAY75091 AAY75092 AAR11061 AAW31706
Escherichia coli E Escherichia coli E Sequence of Plasmo Human prostate can Haemophilus influe Asparagine synthet Drosophila melanog	breas in enc breas in enc acid acid prote prote crgdorf	Mercury-binding re Drosophila melanog Petunia hybrida au Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Orosophila melanog Novel human diagno Amino acid sequenc	Drosophila melanog E. coli cellular p C-terminal portion C-terminal portion C-terminal portion Nelsseria meningit Nelsseria meningit Bovine Coronavirus Bovine coronavirus

ALIGNMENTS

Protein with hemolytic activity, useful for drugs treating jelly fish stings, pharmaceuticals with blood platelet agglutination activity, pesticides by use of the hemolytic activity, and study of the hemolytic mechanism mechanism 01-APR-1998; Carybdea rastonii. Nagai H, (SUNR) SUNTORY LTD. 30-MAR-1999; 07-OCT-1999. WO9950294-Al 1999-580740/49. Nakajima T; 98JP-0088569 99WO-JP01607

Hemolytic protein; blood platelet agglutination; drug development; treatment; sting; jellyfish; pharmaceutical; pesticide.

C. rastonii hemolytic protein derived peptide 2.

06-JAN-2000

(first entry)

AAY33649;

AAY33649 standard; peptide; 18

À

μ.

```
RESULT OF STATE OF ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              뮍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996
01-NOV-1996
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=21094002; E Marchand O., Safi F
        SEQUENCE
                                                                 Synechocystis sp. strain PCC6 entire genome and assignment DNA. Res. 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                              Sugiura M., Tabata S.;
Sugiura M., Tabata S.;
"Sequence analysis of the genome of the unicellular cyanobacterium
"Sequence features in the 1 Mb
Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
Synechocystis sp. strain PCC6803. The genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synechocystis sp. (strain Bacteria; Cyanobacteria; Cyanobacteria; CCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmo salar (Atlantic salmon).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TremBLrel 01-DEC-2001 (TremBLrel THYROID HORMONE RECEPTOR
                                                                                                                                                                   Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nak
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96127529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-PCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                 Kaneko T., Tanaka A., Sato
Sugiura M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q55723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q55723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Molecular cloning in teleost fish.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=8030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TR-BETA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laudet V.
                             iypothetical
                                                                                                                                                                                                                                                             MEDLINE-97061201;
                                                                                                                               Sequence analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GVKETKPEDIGQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GEIQTKPDRVGQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. Endocrinol. 26:51-65(2001)
AF302251; AAL06731.1; -.
                                            D64002; BAA10364.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 7; Conserv
                                                                                                                                                                                                                                                                                   FROM N.A.
                                                                                                                                                                                                                                                                                                                            com map positions 64% 2:153-166(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AUG-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ROM N.A.
    al protein; Complete 476 AA; 50680 km²
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 (TrEMBLrel.
5 (TrEMBLrel.
1 (TrEMBLrel.
1L 50.7 KDA PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
R.,
                                                                                                                                                                                                                                      PubMed=8905231;
., Kotani H., Tanaka
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=8590279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=11174854;
R., Escriva H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (strain PCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13
                                                                                                                               of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45378 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. 01, Created)
1. 01, Last sequence up
1. 19, Last annotation
PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             characterization

    Last sequence update)
    Last annotation update)
    BETA LARGE ISOFORM.

                                                                                  e genome of the unicellular cyanobacterium PCC6803. II. Sequence determination of the ment of potential protein-coding regions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chroococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                     S., Kotani H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 38; DB
Pred. No. 1.2e
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6803).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6F4C1C22AB5DB096 CRC64;
proteome.
935A0C47A73EE6D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Van
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rompaey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of thyroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
on update)
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sazuka T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salmo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prunet
                                                                                                                                                                     Kimura T.,
aruo K., Okumura
da M., Yasuda M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hormone receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Miyajima N.,
                                                                                                                                                                                                                                      Nakamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 φ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                        Σ,
                                                                                                                                                                                          s.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
```

```
В
                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δÃ
                                                                                                                      Q9STM3
                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches
                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                               Matches
                          Q9STM3 PRELIMINARY; PKI; 1970.....
Q9STM3;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE ZINC FINGER PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., DuBois Aldredge T., Bashirzadch R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.; Complete genome sequence of Methanobacterium thermomutotrophicum complete genome sequence of Methanobacterium thermomutotrophicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   deltaH: functional analysis and comparative genomics J. Bacteriol. 179:7135-7155(1997).
-!- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT
                                                                                                                                                                                                                                                                                             PROSITE; PS00198; 4FE4S_FERREDOXIN; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
PATP-binding; Complete proteome; Iron-s
SEQUENCE 623 AA; 69970 MW; 3C04C81
                                                                                                                                                                                                                                                                                                                                                Pfam; PF00005; ABC_tran; Pfam; PF00037; fer4; 1. SMART; SM00382; AAA; 1.
Arabidopsis thaliana (Mouse-ear cress).
Fukarvota; Viridiplantae; Streptophyta;
                                                                                                                                                                                                                                                                                                                                                                                                               (ABC TRANSPORTERS)

EMBL; AE000927; AAB86167.1; -

InterPro; IPR001459; 4Fe4S_ferredoxin.

InterPro; IPR003593; AAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98037514; PubMed=9371463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Methanothermobacter thermautotrophicus. Archaea; Euryarchaeota; Methanobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1998
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     027730
                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003439; ABC_transportr
InterPro; IPR001687; ATP_GTP_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=145262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MTH1695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNASE L INHIBITOR
                                                                                                                                                                          356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      440
                                                                                                                                                                                                                                          Local
                                                                                                                                   15
                                                                                                                                                                                                    N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                \vdash
                                                                                                                                                                          EFKVKPPRVGEA
                                                                                                                                                                                                  EIQTKPDRVGQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GEVRFLPNGDRAGQAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GEIQTKP--DRVGQAT
                                                                                                                                                                                                                              Similarity 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel.
                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY
                                                                                                                                                                          367
                                                                                                                                                                                                    13
                                                                                                                                                                                                                                            58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56
56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14
                                                                                                                                                                                                                                                      .88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 28
                                                                                                                                                                                                                                          . 3¢;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05,
19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence up
Last annotation
                                                                                                                                                                                                                            Score 38; DB
Pred. No. 2e+C
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                             iron-sulfur; Transport
3C04C81278EC135E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                         No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 16;
1.5e+02;
                                                                                                                                                                                                                                                        DВ
  Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A
                                                                                                                                                                                                                                                      17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSPORT PROTEIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Methanobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
                                                                                                                                                                                                                              ω
``
                                                                                                                                                                                                                                                     Length 623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 476;
                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s.
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ij
                                                                                                                                                                                                                            0
```

```
RESULT
Q9W784
                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SQ RIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
Matches
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                           Matches
                                                                                   090Y27
090Y27;
01-DEC-2001
01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9W784;
01-NOV-1999
01-NOV-1999
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a d
the 8 Mb Streptomyces coelicolor
Mol. Microbiol. 21:77-96(1996).
EMBL; AL117385; CAB55654.1; -.
SEQUENCE 425 AA; 44529 MW; E?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmo salar (Atlantic salmon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Chordata; Craniata; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salm
 Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Enkelostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9W784
                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00031; NUCLEAR_RECE DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TR-BETA
                                                           TR-BETA.
                                                                          THYROID
                                                                                                                                                                                                                                                                                                                                                                         Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=8030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THYROID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          245
                                                                                                                                                                                                                   176
                                                                                                                                                                                                                                              ı
                                                                                                                                                                          10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 QTKPDRVGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QQKPDRLGQ 253
                                                                                                                                                                                                                                           GEIOTKPDRVGQA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of H.,
                                                                                                                                                                                                                  GVKETKPEDIGQA
                                                                                                                                                                                                                                                                         Similarity 53.8
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HORMONE
                                                                         HORMONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                               218
218 #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 12, Created)
(TrEMBLrel. 12, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
MONE RECEPTOR BETA (FRAGMENT).
                                                                       (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TREMBLrel. 19, Last annotation updat
(ONE RECEPTOR BETA (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                               AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12
                                                                                                                                                                                                                                                                                                                                              218
25155 MW;
                                                                                                                                                                                                                                                                                        52.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 2%;
                                                                                                                                                                                                                                                                           u
..
                                                                                                                                                                                                                                                                                        Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 39; DB
Pred. No. 88;
                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                       Receptor; Transcription
                                                                                                                                                                                                                                                                        ore 38; DB
Ted. No. 66;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EA0E711A361E992D CRC64;
                                                                                                                                                                                                                                                                                                                                               24802667DC3E843B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              detailed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A3(2)
                                                                                                                                             229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genetic
                                                                                                                                             B
                                                                                                                                                                                                                                                                                                     13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2;
                                                                                     update)
                                                                                                                                                                                                                                                                           Ψ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RECEPTORS FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmo
  Oncorhynchus
                                                                                                                                                                                                                                                                                                    Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and
e.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                           Indels
                             Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             physical map
                                                                                                                                                                                                                                                                                                                                                                                         regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                salmon.";
                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for
                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
 RESULT
Q90Y22
ID Q9
AC Q9
DT 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
Q9PM69
                                                                                                   밁
                                                                                                                           δÃ
                                                                                                                                                                                                                                 A CONTRACTOR OF THE CONTRACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 7
                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15
01-OCT-2000 (TrEMBLrel. 15
01-DEC-2001 (TrEMBLrel. 19
01-DEC-2001 (TrEMBLrel. 19
PUTATIVE ATP/GTP-BINDING P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=21094002; P Marchand O., Safi R Laudet V.;
 Q90Y22
Q90Y22;
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Receptor.
NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                               Complete proteome. SEQUENCE 368 AA;
                                                                                                                                                                                                                                                    InterPro; IPR002744; DUP59.
InterPro; IPR000392; NitrogenaseII.
Pfam; PF01883; DUF59; 1.
Pfam; PF00142; fer4_NifH; 1.
                                                                                                                                                                                                                                                                                                                reveals hypervariable sequences. Nature 403:665-668(2000).
EMBL; AL139079; CAB73594.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Campylobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9PM69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9PM69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF302246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. MOI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular cloning in teleost fish.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=8022;
                                                                                                   146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11
                                                          12
                                                                                                                              44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GEIQTKPDRVGQA
                                                                                                                 GEIQTKPDRVGQ
                                                                                                   GETKTQPEVVGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GVKETKPEDIGQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 7; Conserv
                                                                                                                                                         Similarity 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Endocrinol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1
229
229
 (TrEMBLrel.
                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A
A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=11174854;
R., Escriva H.,
                                                                                                   157
                                                                                                                             12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    229
26357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13
                                                                                                                                                                                                                               40119 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26:51-65(2001).
                                                                                                                                                                        58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52
53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 15,
15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 88
                                                                                                                                                                        . 38
  19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ¥.
  Created
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                       Score
Pred.
                             PRT;
```

```
SEQUENCE FROM N.A.
STRAIN-NCTC 11168;
MEDLINE-20150912; PubMed-10688204;
Parkhill J. Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehaad S., Barrell B.G.;
"The genome sequence of the food borne pathogen Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15, Last sequence update)
19, Last annotation update)
profein (MRP profein HOMOLOG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     epsilon subdivision; Campylobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 38; DB Pred. No. 69; 3; Mismatches
                                                                                    C6AB8AA98A6F7036 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68A25F1428EAE964
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Van
                No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rompaey E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
69;
                   1.1e+02;
                                  DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thyroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRC64;
                              Length 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prunet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             receptors
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
```

æ

```
OGGYLA

OGGYLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (Trew
01-MAY-2000 (Trew
01-MAY-2000 (Trew
CG12588 PROTEIN.
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-BERKELEY;

MEDLINE-20196006; PubNed-10731132;

MEDLINE-20196006; PubNed-10731132;

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R04E5.8.
Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Eukaryota; opoloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;
Pterygota; Neoptera; Endopterygota; Diptera; Brachyce
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9VN53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Direct Submission.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, U41538, AAG00010.1;
InterPro; IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TYEMBLIE). 16, Cree 01-MAR-2001 (TYEMBLIE). 16, Last 01-DEC-2001 (TYEMBLIE). 19, Last 01-DEC-2001 (TYEMBLIE). 19, Last 01-DEC-2001 (TYEMBLIE). 19, Last 01-DEC-2001 (TYEMBLIE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-BRISTOL N2; MEDLINE-99069613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9GYL4
                                                                                                                                                                                                                                                                                                                                                                                                   CG12588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-BRISTOL N2; Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9GYL4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Miller N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-BRISTOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EARPDRIGOA 994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QTKPDRVGQA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -al protein.
997 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DEC-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                              O (TrEMBLrel.
O (TrEMBLrel.
O (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         elegans
) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60
55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                              13,
13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cosmid R04E5.";
EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F1620378EF0D9DB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.4e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   رى
--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhabditida;
                                                                                                                                                                                                                                                                                                                                                                                                                                         update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
                                                                                                                                                                                                                                                                                                                       Brachycera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Consortium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                              Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rhabditoidea;
                                                                                                                                                                                                                                                                                                                    Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
```

```
Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RA DUTBIN K.J. Evangelista C.C. Ferraz C., Ferriera S., Fleischmann W.,
RA DUTBIN K.J. Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Lin X., Mattel B., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA McInulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA McInulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
BMEL, AEO036037272; CG12588.
Soluence 287:185-2195(2000).

BR SEQUENCE 300 AA; 34133 MW; 486855FA0E90ED10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Ma
Best Loc
Matches
STRAIN-A3(2);
STRAIN-97000351; PubMed-8843436;
pedenbach M., Kieser H.M., Denapa
                                                                                           STRAIN=A3(2);
James K.D., Parkhill
Submitted (SEP-1999)
                                                                                                                                                                                                                                                             Streptomyces coelicolor.

Streptomyces coelicolor.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

Bacteria; Firmicutes; Actinobacteria; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                    Q9RL20;
Q9RL20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Burtis K.C., Busam D.A., Butler H., Lauren D., Laures P., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Cherry J.M., Cawley S., Dahlke C., Mays A.D., Dew I., Dietz S.M., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dunkov B.C., Dun Dodson K., Doup L.E., Downes M., Dunan-Rocha S., Fleischman
                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrembLrel. 13, 01-MAY-2000 (TrembLrel. 13, 01-MAY-2000 (TrembLrel. 13, PUTATIVE SECRETED PROTEIN.
                                                                                                                                                                                               STRAIN-A3(2);
Seeger K.J.,
                                                                                                                                                                                                                                                                                                                                  SC5G9.06
                                                              SEQUENCE FROM N.A
                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                 Submitted
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Borkova
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EIOTKPDRVGQAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KMQTKVDAVGQIT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D., Botchan M.R.,
K.C., Busam D.A., I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
X
                                                                                                                                                                              (SEP-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                               Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Benos P.V., Berman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14
                                                                                                                                                                                               D.;
                                                                                              to;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54
61
                                                                                                                                                                              ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Baxendale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 5 %
                                                                                              the EMBL/
                                                                                                                                                                              the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bouck
               Denapaite
                                                                                                                                                                              EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                  Last sequence up
Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В.Р.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                             B.G., Rajandream M.A.;
//GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .P., Bhandari D., Boisman.
.P., Bhandari D., Brottier
., Brokstein P., Brottier
., Cadieu E., Center A., (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39;
No.
               D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                   425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
61;
               Eichner
                                                                                                                                                                                                                                                                                                                                                                                                                                   B
                                                                                                                                                                                                                                                                                                                                                                                   update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŭ
                                                                                                                                                                                                                                                                                                                                                                  update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bolshakov
               Cullum J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chandra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zheng L.,
Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dunn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E).X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      K.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ъ
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Σ.
```

0,

```
RESULT
Q9EQE5
ID Q9
AC Q9
                                                                                                                          g
                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOUR REPORT OF THE PROPERTY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
Q9EQE5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Shah S., Tugendreich S., Forbes D.J.;
"Major Binding Sites for the Nuclear Import Receptor Are the Internal Nucleoportn Nup13 and the Adjacent Nuclear Filament Protein Tpr.";
J. Cell Biol. 141:31-49(1998).
EMBL; AF045567; AAC41273.1;
InterPro; IPR001876; Znf-RanBP.
Pfam; PF00641; Zf-RanBP; S.
SMART; SM00547; ZnF_RBZ; 5.
                                                                                                                                                                                                                                                                                                             01-AUG-1998 (TrEMBLrel. 07, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) NUCLEOPORIN NUP153 HOMOLOG (FRAGMENT).

Xenopus laevis (African clawed frog).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-C57BL/6 SCID; TISSUE-THYMUS; MEDLINE-21040340; PubMed-11196687; Flomerfelt F.A., Kim M.G., Schwartz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
STROMAL PROTEIN ASSOCIATED WITH THYMII AND LYMPH NODES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9EQE4;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9EQE4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Porin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=98198465; PubMed=9531546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISOFORM.
1700021K02RIK OR SPATIAL.
                                                                                                                          175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          639
                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GEIQTKPDRVGQAT
                                                                                                                                                                                                                                                  Match
                                                                                                                                                                 2 EIQTKPDRVGQA
                                                                                                                            EIQPKPDEVGVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSAQTKPDTLSQST
                                                                                                                                                                                                        9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 57...
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1219
                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,
                                                                                                                            186
                                                                                                                                                                   13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14
                                                                                                                                                                                                                          59.7%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.1%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16,
16,
17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MW;
                                                                                                                                                                                                    Score 43; DB Pred. No. 7.5; 0; Mismatches
                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24EB9F96683696F6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197
                     231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
34;
                                                                                                                                                                                                                          DB
7.5;
                     ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                              11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
                                                                                                                                                                                                        Ψ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.
                                                                                                                                                                                                                                              Length 197;
                                                                                                                                                                                                                                                                                                                 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRC64
                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                      depends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SHORT
                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus
                                                                                                                                                                                                                                                                                                                                                                                                                        three-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
```

```
Вb
                 Qy
                                                                                   RESULT
018464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                      δÃ
                                             Query Match
Best Local
                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01826; TIL; 4.
SMART; SM00181; EGF; 4
Signal; Hypothetical p
SIGNAL 1 19
CHAIN 19 337
SEQUENCE 337 AA; 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
STROMAL PROTEIN ASSOCIATED WITH THYMII AND LYMPH NODES LONG
ISOFORM.
1700021K02RIK OR SPATIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                             expressed in the papillae of Dev. Dyn. 0:0-0(1997). EMBL; U82540; AAB67704.1; -
                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Stolidobranchia; Pyu
NCBI_TaxID=7733;
                                                                                                                                                                                                                                                                                      01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
HYPOTHETICAL 35.6 KDA PROTEIN PRECURSOR.
                                                                                                                                                                                                   Arnold J.M., Eri R.,
                                                                                                                                                                                                          STRAIN=CURVATA;
                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                               HMEGFL-1
                                                                                                                                                                                                                                                                                                                             018464;
                                                                                                                                                                                                                                                                                                                                       018464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                       "A novel gene containing
                                                                                                                                                                                                                                                                     Herdmania momus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                          InterPro; IPR000561; EGF-like InterPro; IPR002919; TIL.
270 GNFQCPPDRVGTA
                                                                                                                                                                                                                                                                                                                                                                                      209 EIQPKPDEVGVA
           1 GEIQTKPDRVGQA
                                                                                                                                                                                                                                                                                                                                                                                                       2 EIQTKPDRVGQA
                                                                                                                                                                                                                                                                                                                                                                                                                     u 59.7%;
Similarity 75.0%;
9; Conservative
                                   Similarity 61.88; Conservative
                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Mouse)
                                                                                                                                                                                                                                                 Pyuridae;
                                                                                                                                                                                                                                                                                                                                                                                                       13
                                                                                                                    4.
                 13
282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
Rodentia;
                                                                                                                                                                                                                                                          Chordata;
                                                                                                      protein.
                                                                                   35617
                                             61
                                                                                                                                                                                                 Lavin M.F.;
                                             . 5 %
                                                                                                                                                                                        multiple EGF-like motifs transiently
                                                                                   ¥.
                                                                                                                                                                                of the
                                                                                                                                                                                                                                                  :a; Urochordata; Ascidiacea;
Herdmania.
                                   Score 40; DB pred: No. 45; 0; Mismatches
                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 43; DB Pred. No. 8.9; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                  UNKNOWN PROTEIN.
; 5CCA0924118D8FC6 CRC64;
                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B99BDB8A19BAD71B
                                                                                                                                                                                ascidian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               c stromal cells, its expression.
                                                                                                                                                                                                                                                                                                                                       337
                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
3.9;
                                                                                                                                                                                                                                                                                                                                       Ą
                                                                                                                                                                                tadpole
                                                                                                                                                                                                                                                                                                                                                                                                                                             11;
                                                                                                                                                                                                                                                                                                update)
                                    5
                                                     Length 337;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRC64;
                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        depends
                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        three-
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                          0,
```

RESULT

```
Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Run
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq length: 0 seq length: 2000000000
                 388338833883388378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query
Match
                 100.0
61.1
59.7
55.6
55.6
52.8
52.8
52.8
52.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                June 10, 2002, 15:21:10 ; Search time 58.44 Seconds (without alignments) 41.443 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPTREMBL_19:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       562222 seqs, 172994929 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GEIQTKPDRVGQAT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-647-522-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp_rodent:*
sp_virus:*
sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_archea:*
sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_phage:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp_organelle:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_invertebrate: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_human:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp_fungi:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sp_archeap: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenCore version (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                       Q9GV72
073749
Q9EQE4
Q9EQE5
                                                                                                                                                                                                                                                                                                             018464
Q9GYL4
Q9VN53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IJ
                                                                                                                                                                                                                                                                          Q9RL20
                                                                            Q9W784
Q90Y27
Q9PM69
Q90Y22
Q55723
Q57730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.5
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         562222
                                                                                                                                                                                                                                                                                                                                                                                                   Q9gv72 carybdea ra
O73749 xenopus lae
Q9eqe4 mus musculu
Q9eqe5 mus musculu
09w784 salmo sālar
099y27 oncorhynchu
09pm69 campylobact
090y22 salmo salar
055723 synechocyst
027730 methanother
09stm3 arabidopsis
                                                                                                                                                                                                                                                                       Q9gyl4 caenorhabdi
Q9vn53 drosophila
Q9rl20 streptomyce
                                                                                                                                                                                                                                                                                                                                                                        O18464 herdmania m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
Q96V72
ID Q99
AC Q9
AC 
                                                                                                       RESULT 073749
                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                  Оy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               \begin{array}{c} 117 \\ 128 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\ 138 \\
                                                                                                                                                                                                                                       56
```

ري د	5	36 5	٠ رح	٠ د	ن	UT:	٠ در	٠ ده	u	٠ ت	5	5	ر. در	5	رب ر	5	5	5	5	5	5	5	ر ن	5	5		37 51	. 37 51
.0								.0				.0	.0		. 7	. 4	1.4	. 4	. 4	.4	. 4	. 4	. 4	. 4	. 4	1:4	1.4	.4
																	968 12										79	241 3
			O														2 Q91LG8			Q9X8H7				_	0	õ		Q9P7U7
Q9kpf2 vibrio chol		Q9jx41 neisseria m		O29266 archaeoglob		Q9reg7 bacillus ce	streptom	005492 bacillus ce		Q9s2w5 streptomyce			Ø			trept	Q911g8 white spot	Q91wb7 chenopodium	Q914m3 sulfolobus	strep	3 mus muscul		_	O25067 helicobacte		S	8g73	Q9p7u7 schizosacch

ALIGNMENTS

```
DT AC
                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9GV72
Q9GV72;
01-MAR-2001 (TrEMBLrel. 16, C:
01-MAR-2001 (TrEMBLrel. 16, L:
01-CT-2001 (TrEMBLrel. 18, L:
O73749 PRELIMINARY; PRT;
O73749;
O1-AUG-1998 (TrEMBLrel. 07, Created)
                                                                                                                                                                                                                                                                 "Novel proteinaceous toxins from the box jellyfish (serastoni.";
Biochem. Biophys. Res. Commun. 275:582-588(2000).
EMBL; AB015878; BAB12728.1; -.
SEQUENCE 450 AA; 49392 MW; CD393CF25BEFD2FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Cnidaria; Cubozoa; Cubomedusae; Carybdeidae; Carybdea.`
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carybdea rastonii.
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=20422301; PubMed=10964707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOXIN-1.
                                                                                                                                                                                                                                                                                                                                                     Nakajima T.;
                                                                                                                                                                                                                                                                                                                                                                 Nagai H., Takuwa K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=78582;
                                                                                                                                     1 GEIQTKPDRVGQAT 14
                                                                                                                     GEIQTKPDRVGQAT 69
                                                                                                                                                                                    Conservative
                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                 Nakao M., Ito E., Miyake M., Noda M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                    0
                                                                                                                                                                                 Score 72; DB 5;
Pred. No. 0.00011;
, Mismatches 0;
                                       1219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                450
                                       ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Å
                                                                                                                                                                                                                Length 450;
                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                  (sea wasp) Carybdea
                                                                                                                                                                                 0;
                                                                                                                                                                                   Gaps
                                                                                                                                                                                 0
```

modified

non-profit institutions and this statement is not

ons as long not removed.

as its content Usage

Š

þу

and

for in

commercial no

```
SQ TITLE TO THE TENT OF THE TE
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THB_PAROL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THB_PAROL Q91279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities re
or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X61236; CAA43554.1;
                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleost Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes; Pleuronectoidei; Paralichthyidae; Paralichthys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00169; PH; 1.
SMART; SM00233; PH; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thyroid hormone receptor beta (THR-beta). THRB OR NR1A2.
                                                                                                                                                                                                  -i- I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Paralichthys olivaceus (Flounder).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-96149097; PubMed=8536930;
Yamano K., Inul Y.;
                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=8255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence u
15-JUL-1999 (Rel. 38, Last annotation
                                                                                                                                                                                                                                                                   flounder.";
                                                                                                                                                                                                                                                                                     "cDNA cloning of thyroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 58.1 tes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 IQTKPDRVGQAT 14
                                                                                          INDET:,

Comp. Endocrinol. 99:197-203(1995).

Comp. Endocrinol. 99:197-203(1995).

FUNCTION: HIGH AFFINITY RECEPTOR FOR TRIIODOTHYRONINE.

SUBCELLULAR LOCATION: Nuclear.

SUBCELLULAR LOCATION: Nuclear.

ALTERNATIVE PRODUCTS: 2 ISOFORMS; BETA-1 (SHOWN HERE) AND BETA-2;

SEEM TO BE PRODUCED BY ALTERNATIVE SPLICING.

SEEM TO BE PRODUCED BY ALTERNATIVE SPLICING N-TERMINAL DOMAIN,

DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,

DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATION DOMAIN.
                                                                                   A DNA-BINDING DOMAIN AND A C-TERMINAL SIMILARITY: BELONGS TO THE NUCLEAR HO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S0002557; NUM1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LTTKEDKKGQAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR001849; PH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S19052.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1384
656
727
798
862
926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        990
1054
1118
1182
1182
1246
1310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PH_DOMAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           313202
                                                                                                                                                                                                                                                                                            hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ψ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.
9.
10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (INCOMPLETE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B2FBD67C9F6211AE CRC64;
                                                                                                                                                                                                                                                                                            receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TANDEM REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
3.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA
                                                                                                                                                                                                                                                                                            beta
                                                                                                                                                                                                                                                                                            for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                            the Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neoteleostei;
                       a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
```

of

EMBL

outstation

```
Š
밁
                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA_BIND
ZN_FING
ZN_FING
                                                                                                                                                                                               (1)
SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE-94089392; PubMed-8265357;
MEDLINE-94089392; PubMed-8265357;
                                                                                                                                                                                                                                                                                                                                                                     HYDH_ECOLI P14377;
                                                                                                                                                                                                                                                                                                                                                                                            _ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00104; hormone_rec; Pfam; PF00105; zf-C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D45245;
HSSP; P10828;
                                                                       MEDLINE=89327164; PubMed=2666400;
Stoker K., Reijnders W.N.M., Oltmann L.F., Stouthamer A.H.;
"Initial cloning and sequencing of hydHG, an operon homologous
ntrBC and regulating the labile hydrogenase activity in Escheri
                                                                                                                                                                                                                                                                                                                    01-JAN-1990 (Rel. 13, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Sensor protein hydH (EC 2.7.3.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor; Tra
Zinc-finger;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00430; HOLI; 1.
SMART; SM00399; ZnF_C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00398; STRDHORMONER. PRINTS; PR00047; STROIDFINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001628; zf-C4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this
                                                                                                                                                                                                                                                                                                  Escherichia
                                                                                                                                                                                                                                                                                                              HYDH OR B4003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                              J. Bacteriol.
                                                                   coli K-12.
                                                                                                                            STRAIN-K12
                                                                                                                                                                       "Analysis of the region from 89.2
                                                                                                                                                                                              Daniels D.
                                                                                                                                                                                                                                                                             Escherichia
                                                                                                                                                                                                                                                                                        Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                      SEQUENCE OF 328-465 FROM N.A.
                                                                                                                                                                                                                                                               NCBI_TaxID=562;
                                                                                                                                                             Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                        175
          FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATIORY SYSTEM HYDH/HYDG INVOLVED IN THE REGULATION OF THE LABILE HYDROGENASE ACTIVITY HYDH MAY FUNCTION AS A MEMBRANE-ASSOCIATED PROTEIN KINASE THAT PHOSPHORYLATES HYDG IN RESPONSE TO ENVIRONMENTAL SIGNALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    European Bioinformatics Institute.
 SUBCELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GEIQTKPDRVGQAT
                                                                                                                                                                                                                                                                                                                                                                                                                                        GVKEDKPEEIGQAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS00031; NUCLEAR_RECEPTOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    requires
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transcription regulation; DNA-bin er; Multigene family; Alternative MODULATING.

31 MODULAR RECEPT 32 99 NUCLEAR RECEPT 32 52 C4-TYPE.

70 94 C4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR000536; Hormone_rec_lig
IPR001723; Strdhormone_rec
                                                                                                                                                                                                                                                                                      Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           395
                                                                                                                                                                                                                                                                                                 coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1
32
32
70
149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -profit
                                                       171:4448-4456(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BAA08201.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                           Escherichia coli genome.
to 92.8 minutes.";
s. 21:5408-5417(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                        188
                                                                                                                                                                                                                                                                                                                                                                                                                                                             14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   license
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strdhormone_receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WW.
                                                                                                                                                                                                                                                                                      gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 35; DB Pred. No. 63; 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIGAND-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEAR RECEPTOR-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F4319CDF96FE2451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        There are no rest
                                                                                                                                                                                                         III,
                                                                                                                                                                                                                                                                                                                                                                                A
                                                                                                                                                                                   IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>, .</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Usage
                                                                                                                                                                                                          Sofia H.J.,
                                                                                                                                                                                   DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              γď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and
                                                                              Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                commerc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               its
way
ial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
```